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DEFINITION    Sequence 1 from Patent WO2004026772.
ACCESSION     CQ796908
VERSION       CQ796908.1 GI:46408534
KEYWORDS      unidentified
              unidentified
              unclassified sequences.
SOURCE        ORGANISM
              Hovaneec, T. A.
              Ammonia-oxidizing bacteria and methods of using and detecting
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Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 LOCUS Sequence 1 from Patent EP1502948.
 DEFINITION CS089154
 ACCESSION CS089154
 VERSION CS089154.1 GI:66714438
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE
 1 Hovanec, T. A. and Burrell, P. C.
 AUTHORS Ammonia-oxidizing bacteria
 TITLE Patent: EP 1502948-A 1 02-FEB-2005;
 JOURNAL Aquaria Inc. (US)
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 Best Local Similarity 100.0%; Pred. No. 8.3e-16;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
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 DEFINITION Sequence 2 from Patent EP1502948.
 ACCESSION CS089155
 VERSION CS089155.1 GI:6714439
 KEYWORDS
 SOURCE unidentified

ORGANISM unidentified
 unclassified.
 REFERENCE 1
 AUTHORS Hovanec, T.A. and Burrell, P.C.
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 Best Local Similarity 100.0%; Pred. No. 8.3e-16;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS      AXJ16093      1457 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION      Sequence 2 from Patent W00190312.
ACCESSION      AXJ16093
VERSION      AXJ16093.1      GI:117899284
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SOURCE      unidentified
ORGANISM      unidentified

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REFERENCE      1
AUTHORS      Hovanes, T. A. and Burrell, P. C.
TITLE      Ammonia-oxidizing bacteria
JOURNAL      Patent: WO 0190312-A 2 29-NOV-2001;
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ORIGIN
Query Match      100.0%; Score 1457; DB 6; Length 1457;
Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      181 GACCTTGCGCTTTGGAGCGCGCATGCTGATTAGTCTAGTTGGTGGGTTAAAGGCTTAC 240
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Qy      661 TGAATGCGTAGAGATATGAAAGAACATGATGCGAAGGCGACGCTCTGGGTAAACACT 720
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Qy      841 AGTTGACCGCTGGGAGATCGGTGCGAAAGATTAAACCTCAAGAGAAATTGACGGGACCC 900
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Qy      1261 TCGTAGTCCGGAATCGGAGTCTGCAACTCCGCTGTGAAGTCCGAATTCGTATATCCG 1320
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QY 1321 GATCAGCATGTCGCGGTGAATACGTTCCCGGCTTTGTACACACCGCCCGTCAACAT 1380
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 QY 1441 GATTCACTGCTGGGGTG 1457
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 LOCUS Nitrosomonas sp. R7c131 16S ribosomal RNA gene, partial sequence.
 ACCESSION AF386752
 VERSION AF386752.1 GI:17864829
 KEYWORDS ENV.
 SOURCE Nitrosomonas sp. R7c131
 ORGANISM Nitrosomonas sp. R7c131
 Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 Nitrosomonadaceae; Nitrosomonas; environmental samples.
 REFERENCE
 AUTHORS 1 (bases 1 to 1457)
 TITLE Identification of bacteria responsible for ammonia oxidation in
 freshwater aquaria
 JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
 PUBMED 11722936
 REFERENCES 2 (bases 1 to 1457)
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.
 TITLE Direct Submision
 JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria
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 Best Local Similarity 99.9%; Pred. No. 8.8e-16;
 Matches 1456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 541 AAAGGTGGCAGAGCGGCTTTGTAACTGATGATGTAATCCCGGCTTAATCTGGGAAT 600
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LOCUS      CQ796909              1457 bp      DNA      linear      PAT 19-APR-2004
DEFINITION Sequence 2 from Patent WO2004026772.
ACCESSION  CQ796909
VERSION     CQ796909.1 GI:46408535
KEYWORDS
SOURCE      unidentified
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            unclassified sequences.
REFERENCE   1
AUTHORS     Hovanec, T. A.
TITLE       Ammonia-oxidizing bacteria and methods of using and detecting
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Query Match      99.7%; Score 1457.2; DB 6; Length 1457;
Beef Local Similarity 99.8%; Pred. No. 9.8e-16;
Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      121 AGGCATCGAAGATGCTAATACCGCATATCTTAAGAGGAGAAAGAGGGGATCGAAA 180
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Qy      241 CAAGGCGACATCACTAGTGTCTGAGAGAGACCAAGCCACACTGGGACTGAGACAG 300
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Qy      361 CAGCAATGCGCGGTAGTGAAGAGGCTTCGGGTGTAAAGCTCTTTGAGTGCAGAGAA 420
Db      361 CAGCAATGCGCGGTAGTGAAGAGGCTTCGGGTGTAAAGCTCTTTGAGTGCAGAGAA 420
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Qy      481 TAGGTGCGACAGCGCGGTAATAGTAGGGTGCAGAGCGTTATCGAAATTAATCTGGGCGT 540
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Db      541 AAAGGTGGCGAGGCGGCTTTGTAACTGAGATGTGAATCCCGGGCTTAACCTGGGAAT 600
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Db      601 TCGCTTTGAACCTACAGGCTAGATGGGCGAGAGGGGTGAATTCATGATGTGACAG 660
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RESULT 9
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LOCUS      AF386757
DEFINITION Nitrosomonas sp. R7c187 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF386757
VERSION     AF386757.1 GI:17864834
KEYWORDS   ENV.
SOURCE      Nitrosomonas sp. R7c187
ORGANISM   Nitrosomonas sp. R7c187

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Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas; environmental samples.

REFERENCE 1 (bases 1 to 1457)
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.
 TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria
 JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
 PUBMED 11729336
 REFERENCE 2 (bases 1 to 1457)
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr., Moorpark, CA 93021, USA
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 Best Local Similarity 99.7%; Pred. No. 1.1e-15;
 Matches 1452; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 ACCESSION AF386751 GI:17864828
 VERSION AF386751.1 GI:17864828
 KEYWORDS ENV.
 SOURCE Nitrosomonas sp. R7c155
 ORGANISM Nitrosomonas sp. R7c155
 Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas; environmental samples.
 REFERENCE 1 (bases 1 to 1426)
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.
 TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria

JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
 PUBMED 11722936
 REFERENCE 2 (bases 1 to 1426)
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr., Moorpark, CA 93021, USA
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Query Match 97.3%; Score 1417; DB 3; Length 1426;
 Best Local Similarity 99.5%; Pred. No. 3.6e-15;
 Matches 1420; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 61 CATCGGACGTATCCAGAGAGAGGGGGTAAACGATGAAAGATGTCTTAATACCGCAT 120
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Oy 692 TGGCGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
Db 661 TGGCGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Oy 752 CAGGATTAGATACCTGTAGTTCACGCGCTTAAAGATGTCAATAGTTTGGGCTTAA 811

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Db 721 CAGGATTAGATACCTGTAGTTCACGCGCTTAAAGATGTCAATAGTTTGGGCTTAA 780
Oy 812 TTAGGCTGTGTAACGAAGCTTAACGGGTGAAGTTGACCGGCTGGGAGATACCGTAAGA 871
Db 781 TTAGGCTGTGTAACGAAGCTTAACGGGTGAAGTTGACCGGCTGGGAGATACCGTAAGA 840
Oy 872 TTAAGCTCAAGAGATTAACGGGAGACCGGACCAAGCGGTGATTAATGATTAATTCG 931
Db 841 TTAAGCTCAAGAGATTAACGGGAGACCGGACCAAGCGGTGATTAATGATTAATTCG 900
Oy 932 ATGCAACGGGAAAACTTACCTCACTTTGACATGATGCAATTTTCTAGAGATTAATTA 991
Db 901 ATGCAACGGGAAAACTTACCTCACTTTGACATGATGCAATTTTCTAGAGATTAATTA 960
Oy 992 GTGCTTCGGGAAACGTTACACAGAGTGTGATGCTGTCACGCTGCTGCTGCTGAGATG 1051
Db 961 GTGCTTCGGGAAACGTTACACAGAGTGTGATGCTGTCACGCTGCTGCTGCTGAGATG 1020
Oy 1052 TTGGGTTAAGTCCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1111
Db 1021 TTGGGTTAAGTCCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Oy 1112 ACTTTAATGAGATGCTCCGGTGAACAAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1171
Db 1081 ACTTTAATGAGATGCTCCGGTGAACAAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Oy 1172 GGGCTTATGGGTAGAGGCTTACACAGTAAATACATGAGGCGGTACAGAGGTTGCCAACCC 1231
Db 1141 GGGCTTATGGGTAGAGGCTTACACAGTAAATACATGAGGCGGTACAGAGGTTGCCAACCC 1200
Oy 1232 GCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1291
Db 1201 GCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Oy 1292 TCCGTGAAGTGGAAATGCTAGTAATTCGCGATGACATGTCGCGTGAATACGTTCCCG 1351
Db 1261 TCCGTGAAGTGGAAATGCTAGTAATTCGCGATGACATGTCGCGTGAATACGTTCCCG 1320
Oy 1352 GGTCTTTGACACACCGCCCGTACACCATGAGAGTGGTTTTCACAGAGAGAGATGAT 1411
Db 1321 GGTCTTTGACACACCGCCCGTACACCATGAGAGTGGTTTTCACAGAGAGAGATGAT 1380
Oy 1412 AACCGTAAGAGAGGCGCTTGGCCAGGTGAGATTCAATGATGGGGTG 1457
Db 1381 AACCGTAAGAGAGGCGCTTGGCCAGGTGAGATTCAATGATGGGGTG 1426

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RESULT 11
 AF386746 1487 bp DNA linear ENV 10-MAY-2004
 LOCUS Nitrosomonas sp. Bf16c57 16S ribosomal RNA gene, partial sequence.
 DEFINITION AF386746
 ACCESSION AF386746.1 GI:17864823
 VERSION ENV.
 KEYWORDS Nitrosomonas sp. Bf16c57
 SOURCE Nitrosomonas sp. Bf16c57
 ORGANISM Nitrosomonas sp. Bf16c57
 Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 Nitrosomonadaceae; Nitrosomonas; environmental samples.
 REFERENCE 1 (bases 1 to 1487)
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.
 TITLE Identification of bacteria responsible for ammonia oxidation in
 JOURNAL freshwaters aquaria
 PUBMED Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
 REFERENCE 11722936
 AUTHORS 2. (bases 1 to 1487)
 Burrell, P.C., Phalen, C.M. and Hovanec, T.A.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria
 GROUP, 6100 Condon Dr., Moorpark, CA 93021, USA
 FEATURES Location/Qualifiers
 source 1. 1487
 /organism="Nitrosomonas sp. Bf16c57"


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/isolation_source="ammonia-oxidizing bacteria isolated
from freshwater aquaria enrichments"
/db_xref="taxon:180505"
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/product="16S ribosomal RNA"

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ORIGIN
Query Match      95.5%; Score 1391.6; DB 3; Length 1487;
Best Local Similarity 97.6%; Pred. No. 8.5e-15;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCAGACGCGATGCTTGCAT 60
DB 18 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCAGACGCGATGCTTGCAC 77
QY 61 CTGGTGGCGAGTGGCGGAGTGAATGCAATGCGAAGCTATCCAGAAAGAGGGGGTA 120
DB 78 CTGGTGGCGAGTGGCGGAGTGAATGCAATGCGAAGCTATCCAGAAAGTGGGGATA 137
QY 121 ACCGATCGAAAGATGCTATATACCGCATATCTTAAAGAGGAAACAGGGGATCGAAA 180
DB 138 AGCGATCGAAAGATGCTATATACCGCATATCTTAAAGAGGAAACAGGGGATCGAAA 197
QY 181 GACCTTGGCGTTTGGAGCGCGCGATGCTGATTAAGTATGTTGGGGTTAAAGCTTAC 240
DB 198 GACCTTGGCGTTTGGAGCGCGCGATGCTGATTAAGTATGTTGGGGTTAAAGCTTAC 257
QY 241 CAAGGCGAGATGATGATGCTGAGAGAGACGACGACACCTGGGACTGAGACAG 300
DB 258 CAAGGCGAGATGATGATGCTGAGAGAGACGACGACACCTGGGACTGAGACAG 317
QY 301 GCCCAGACTCTTACGCGAGGACAGCAGTGGGAAATTTTGGACAAATGGCGCGAACCTGATC 360
DB 318 GCCCAGACTCTTACGCGAGGACAGCAGTGGGAAATTTTGGACAAATGGCGCGAACCTGATC 377
QY 361 CAGCAATGCCCGTGAAGTGAAGAGCGCTTGGGGTTGTAAGCTCTTTCAGTGAAGAGA 420
DB 378 CAGCAATGCCCGTGAAGTGAAGAGCGCTTGGGGTTGTAAGCTCTTTCAGTGAAGAGA 437
QY 421 AAAAGGTACGGTAAATTAATGTCATGACGATTCGACAGAAAGACACCGGCTAAC 480
DB 438 AAAAGGTACGGTAAATTAATGTCATGACGATTCGACAGAAAGACACCGGCTAAC 497
QY 481 TAGCTCCAGACACCGCGGTAATACGTAAGGTGCAAGCTTAATCGAATTAATCGGCGCT 540
DB 498 TAGCTCCAGACACCGCGGTAATACGTAAGGTGCAAGCTTAATCGAATTAATCGGCGCT 557
QY 541 AAAAGGTGCGAGCGCGCTTGTAAAGTCAAGTGAATCCCGGGCTTAACCTGGGAAT 600
DB 558 AAAAGGTGCGAGCGCGCTTGTAAAGTCAAGTGAATCCCGGGCTTAACCTGGGAAT 617
QY 601 TGGGTTTGAACATCAAGGCTAGAGTGGCAAGAGGAGTGAATCCATGTTGAGCAG 660
DB 618 TGGGTTTGAACATCAAGGCTAGAGTGGCAAGAGGAGTGAATCCATGTTGAGCAG 677
QY 661 TGAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGCAGCTTCTGGTTAACT 720
DB 678 TGAATGCGTAGAGATATGGAAGAACATCGATGGCGAAGCAGCTTCTGGTTAACT 737
QY 721 GACGCTCATGACGAAGAGCGTGGGAGCAAAACAGATTAAATCCCTGTATGTCACGCC 780
DB 738 GACGCTCATGACGAAGAGCGTGGGAGCAAAACAGATTAAATCCCTGTATGTCACGCC 797
QY 781 CTAAGAGATGCAATAGTGTGGGCTTAATAGGCTTGTGTAACGAAGCTAACGCGTGA 840
DB 798 CTAAGAGATGCAATAGTGTGGGCTTAATAGGCTTGTGTAACGAAGCTAACGCGTGA 857
QY 841 AGTTGACCGGCTGGGAGTACGCTGCGAAGATTAAAACCTAAAGGAATTGACGGGGACCC 900
DB 858 AGTTGACCGGCTGGGAGTACGCTGCGAAGATTAAAACCTAAAGGAATTGACGGGGACCC 917

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QY 901 GCACAAGCGGTGATTAATGATTAATTCATGCAACGCGAAGAAACCTTACTACCTT 960
DB 918 GCACAAGCGGTGATTAATGATTAATTCATGCAACGCGAAGAAACCTTACTACCTT 977
QY 961 GACATGTACGGAATTTCTAGAGATAGATTAGTG-CTTCGGAAACGCTTAACACAGTGTCT 1019
DB 978 GACATGTACGGAATTTCTAGAGATAGATTAGTG-CTTCGGAAACGCTTAACACAGTGTCT 1037
QY 1020 GCATGGCTGTGCTCAGCTGTGTGCTGAGATGTTGGGTTAAATCCCGCAACGAGCGAAC 1079
DB 1038 GCATGGCTGTGCTCAGCTGTGTGCTGAGATGTTGGGTTAAATCCCGCAACGAGCGAAC 1097
QY 1080 CCTTGTCATTAAATGCGCATCATTTGGTGGGCACTTAAATGAGACTGCGGAGCAAAAC 1139
DB 1098 CCTTGTCATTAAATGCGCATCATTTGGTGGGCACTTAAATGAGACTGCGGAGCAAAAC 1157
QY 1140 GGAGGAGGTGGGAGTGAAGTCAAGTCAAGTCTCATGAGCCCTTATGAGGCTTACACGTA 1199
DB 1158 GGAGGAGGTGGGAGTGAAGTCAAGTCAAGTCTCATGAGCCCTTATGAGGCTTACACGTA 1217
QY 1200 ATACAAATGCGGCTACAGAGGTTGCCAACCCGCGAGGGAGGCTTAATCTCAAGAAACCC 1259
DB 1218 ATACAAATGCGGCTACAGAGGTTGCCAACCCGCGAGGGAGGCTTAATCTCAAGAAACCC 1277
QY 1260 GTGTGATGCGGATGCGAGTCTGCAACTGACTCCGTAAGTCGGAATGCTAGTAATCG 1319
DB 1278 GTGTGATGCGGATGCGAGTCTGCAACTGACTCCGTAAGTCGGAATGCTAGTAATCG 1337
QY 1320 CGGATCAGCATGTCGGGCTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTACACCA 1379
DB 1338 CGGATCAGCATGTCGGGCTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTACACCA 1397
QY 1380 TGGAGTGGGTTTACACAGAACAGAGTACTCTAACCTTAAGAGAGGCGCTTGGCAAGGTG 1439
DB 1398 TGGAGTGGGTTTACACAGAACAGAGTACTCTAACCTTAAGAGAGGCGCTTGGCAAGGTG 1457
QY 1440 AGATTGATGACTGGGGTG 1457
DB 1458 AGATTGATGACTGGGGTG 1475

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RESULT 12
CQ796927      1491 bp      DNA      linear      PAT 19-APR-2004
LOCUS         CQ796927
DEFINITION   Sequence 20 from Patent WO2004026772.
ACCESSION    CQ796927
VERSION      CQ796927.1 GI:46408553
KEYWORDS
SOURCE       unidentified
              unidentified
              unclassified sequences.
ORGANISM     Hovaneec, T. A.
REFERENCE    1
AUTHORS      Ammonia-oxidizing bacteria and methods of using and detecting
              thesame
TITLE        Patent: WO 2004026772-A 20 01-APR-2004;
JOURNAL      Aquaria Inc. (US)
FEATURES     Location/Qualifiers
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ORIGIN

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Query Match      95.5%; Score 1391.6; DB 6; Length 1491;
Best Local Similarity 97.6%; Pred. No. 8.5e-15;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCAGACGCGATGCTTGCAT 60
DB 18 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCAGACGCGATGCTTGCAC 77

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OY 61 CTGGTGGCCAGTGGCCGAGCGGTGAGTAATGCAATCGGAAGCTATCCAGAAAGAGGGGGGTA 120
DB 78 CTGGTGGCCAGTGGCCGAGCGGTGAGTAATGCAATCGGAAGCTATCCAGAAAGAGGGGGGTA 137
OY 121 AGCATCGAAAGATGTCTAATATACCGCATTAATCTTAAGAGAGAAAGAGGGGATCGAAA 180
DB 138 AGCATCGAAAGATGTCTAATATACCGCATTAATCTTAAGAGAGAAAGAGGGGATCGAAA 197
OY 181 GACCTTGGCCCTTTGGAGCGGCGGATGTCTGATTAAGCTAGTTGGTGGGGTAAAGGCTTAC 240
DB 198 GACCTTGGCTTTGGAGCGGCGGATGTCTGATTAAGCTAGTTGGTGGGGTAAAGGCTTAC 257
OY 241 CAAGGAGAGATCAATAGTGTCTGAGAGAGAGACACGACACATCGGAGCTGAGACAG 300
DB 258 CAAGGAGAGATCAATAGTGTCTGAGAGAGAGACACGACACATCGGAGCTGAGACAG 317
OY 301 GCCCAGACTCTTACGGGAGGACAGTGGGGAATTTTGGACAATGGGCGCAAGCTGATC 360
DB 318 GCCCAGACTCTTACGGGAGGACAGTGGGGAATTTTGGACAATGGGCGCAAGCTGATC 377
OY 361 CAGCAATGCCCGCGTGAAGTAAGAGGCTTGGGTTGTAAGCTCTTTCAGTGAAGAGA 420
DB 378 CAGCAATGCCCGCGTGAAGTAAGAGGCTTGGGTTGTAAGCTCTTTCAGTGAAGAGA 437
OY 421 AAAGGTTAGGTAATATCTGATCTATGACGCTATCGACAGAAAGACCGGCTAAC 480
DB 438 AAAGGTTAGTATTAATCAACAATTAATGACGCTATCGACAGAAAGACCGGCTAAC 497
OY 481 TAGGTGCGACAGCGCGGTAATACGTAAGGGTGCAGAGCGTAAATTCGAAATTAATCGGAGCT 540
DB 498 TAGGTGCGACAGCGCGGTAATACGTAAGGGTGCAGAGCGTAAATTCGAAATTAATCGGAGCT 557
OY 541 AAAGGTTGCGACAGCGCGCTTTGTAGTCAAGTGTGAATCCCGGGCTTAACTCGGGAAT 600
DB 558 AAAGGTTGCGACAGCGCGCTTTGTAGTCAAGTGTGAATCCCGGGCTTAACTCGGGAAT 617
OY 601 TGGCTTTGAATCAACAAGCTAGAGTGTGCGACAGAGGAGTGAATTCATGTGTAGCAG 660
DB 618 TGGCTTTGAATCAACAAGCTAGAGTGTGCGACAGAGGAGTGAATTCATGTGTAGCAG 677
OY 661 TGAATAGCGTAGATATGAAAGAAATCATGATGGCGAAGGACCTCTGGGTTAACACT 720
DB 678 TGAATAGCGTAGATATGAAAGAAATCATGATGGCGAAGGACCTCTGGGTTAACACT 737
OY 721 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGATTAAGATACCTGTGTAGTCACGCC 780
DB 738 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGATTAAGATACCTGTGTAGTCACGCC 797
OY 781 CTAAACGATGCAACTAGTGTGTTGGGCTTATTAAGCTTGTGTAACGAACCTAACCGGTGA 840
DB 798 CTAAACGATGCAACTAGTGTGTTGGGCTTATTAAGCTTGTGTAACGAACCGGTGA 857
OY 841 AGTTGACCGCTGGGAGTACGGTCCGAAGATTAAACTCAAGGAATTGACGGGAGACC 900
DB 858 AGTTGACCGCTGGGAGTACGGTCCGAAGATTAAACTCAAGGAATTGACGGGAGACC 917
OY 901 GCACAAAGCGGTGATTAATGTGATTAATTCGATGCAACCGGAAAACCTTAACCTACCTT 960
DB 918 GCACAAAGCGGTGATTAATGTGATTAATTCGATGCAACCGGAAAACCTTAACCTACCTT 977
OY 961 GACATGTAGCGAATTTCTAGAGATAGATTAGTG-CTTGGGGAAGCGCTAACACAGGTGCT 1019
DB 978 GACATGTAGCGAATTTCTAGAGATAGATTAGTG-CTTGGGGAAGCGCTAACACAGGTGCT 1037
OY 1020 GCATGGCTGTGTCAGCTGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGACGCAAC 1079
DB 1038 GCATGGCTGTGTCAGCTGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGACGCAAC 1097
OY 1080 CTTGTGATTAATGTCATCAATTTGGTGGGCACTTAAATGAGACTGCGGGTGAACAAC 1139
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OY 1140 GGAGAGAGTGGGAGATGACGTCAAGTCCCTATGAGCCCTTATGGGTAGGGCTTCAACGTA 1199
DB 1158 GGAGAGAGTGGGAGATGACGTCAAGTCCCTATGAGCCCTTATGGGTAGGGCTTCAACGTA 1217
OY 1200 ATACATGCGCGCTACAGAGGTTGCCAACCCCGCAGAGGGGAGCTAATCTCAAGAAAGCCG 1259
DB 1218 ATACATGCGCGCTACAGAGGTTGCCAACCCCGCAGAGGGGAGCTAATCTCAAGAAAGCCG 1277
OY 1260 GTCTGATGTCGGATGAGGATCTGCAACTGATCCGTGAAGTCGGAATGCTTAATGTA 1319
DB 1278 GTCTGATGTCGGATGAGGATCTGCAACTGATCCGTGAAGTCGGAATGCTTAATGTA 1337
OY 1320 CGATACAGATGTCGGGTAATAGTTCGCGGGTCTTGTAACAACCGCGCTCAACCA 1379
DB 1338 CGATACAGATGTCGGGTAATAGTTCGCGGGTCTTGTAACAACCGCGCTCAACCA 1397
OY 1380 TGGGAGTGGGTTTCAACGAAGCAGATGATTAACCGTAAGAGGAGCGCTTCCACGCTG 1439
DB 1398 TGGGAGTGGGTTTCAACGAAGCAGATGATGTTAACCGTAAGAGGAGCGCTTCCACGCTG 1457
OY 1440 AGATTCAATGACTGGGCTG 1457
DB 1458 AGATTCAATGACTGGGCTG 1475

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RESULT 13
AJ621032 1445 bp DNA linear BCT 08-JUN-2004
LOCUS Nitrosomonas sp. Is343 16S rRNA gene, isolate Is343.
DEFINITION AJ621032
ACCESSION AJ621032
VERSION AJ621032.1 GI:40994851
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Nitrosomonas sp. Is343
ORGANISM Nitrosomonas sp. Is343
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.

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REFERENCE 1
Bollmann, A., Schmidt, I. and Bodelier, P.L.E.
Influence of salt on activity, growth, protein pattern and fatty
acid composition of the new isolated ammonia oxidizing strain
Nitrosomonas strain Is343
Unpublished
2 (bases 1 to 1445)

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JOURNAL Direct Submission
AUTHORS Submitted (15-JUN-2004) Bollmann A., Department for Microbial
Ecology, NIOO-KNAW Centre for Limnology, Rijksstraatweg 6, 3631 AC
Nieuwersluis, NETHERLANDS
JOURNAL

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source location/Qualifiers
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/mol_type="genomic DNA"
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/isolation_source="brakish water"
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ORIGIN

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Query Match 95.4%; Score 1390.6; DB 1; Length 1445;
Best Local Similarity 98.5%; Pred. No. 9.1e-15;
Matches 1424; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

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OY 5 AACGTGGCGGCAATGCTTATACATGCAATGCAAGTGAACGCGACAGCGATGCTGCACTGG 64
DB 1 AACGTGGCGGCAATGCTTATACATGCAATGCAAGTGAACGCGACAGCGATGCTGCACTGG 60
OY 65 TGGCAGTGGCGGACGCGGTGAGTAATGATCGGAACGTATCCAGAAAGAGGGGGGTAAAGC 124

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Db	61	TGGCGAGTGGCGGACGGGTGAGTAATTAATCTGGAACTGATCCAGAACTGATCCAGAAAGGGGGATTAACGC	120
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Db	121	ATCGAAAAGATGTCTTAATAACCGCATATATCTCTGAAGAGAAAAGCGGGGATTCGAAAAGCC	180
Qy	185	TTGGCGCTTTTGAAGCGCCGATGTGTCTGAATTAGCTGATGTGTGGGGTTAAAGGCTTCCAAAG	244
Db	181	TTGGCGCTTTGGGAGCGCCGATGTGTGAATTAGCTGATGTGTGGGGTTAAAGGCTTCCAAAG	240
Qy	245	GCGACGATCAGTATGTTGGTCTGAGAGAGACGACACGCCACACTGGGACTGAGACACGCGCC	304
Db	241	GCGACGATCAGTATGTTGGTCTGAGAGAGACGACACGCCACACTGGGACTGAGACACGCGCC	300
Qy	305	AGACTCTTACCGGAGGACGACAGTGGGAAATTTTGGACAAATGGCGCAAGCTGATCCAGC	364
Db	301	AGANTCTTACCGGAGGACGACAGTGGGAAATTTTGGACAAATGGCGCCAGACCTGATCCAGC	360
Qy	365	AATCCCGGTGATGTAAGAAGGCCCTTCGGGTGTGAACCTCTTTCAGTCCAGAAAGAAAG	424
Db	361	AATCCCGGTGATGTAAGAAGGCCCTTCGGGTGTGAACCTCTTTCAGTCCAGAAAGAAAG	419
Qy	425	GTTACGGTAAATTAATCGTACCTCATGACGGTATCGACAGAAAGACACCGGCTAACTCAG	484
Db	420	GCTGACGTGAATTACTGTAGTTCTATGACGGTATCGACAGAAAGACACCGGCTAACTCAG	479
Qy	485	TGCCAGACCGCGCGTAAATCGTAAAGGTGCAGCGCTTAATCGAAATTACTGGCGCTAAAG	544
Db	480	TGCCAGACCGCGCGTAAATCGTAAAGGTGCAGCGCTTAATCGAAATTACTGGCGCTAAAG	539
Qy	545	GGTGCGCAGCGCGCTTTGTAAGTCAAGATGTAAATCCCCGGGCTTAACCTGGGAATTGCG	604
Db	540	GGTGCGCAGCGCGCTTTGTAAGTCAAGATGTAAATCCCCGGGCTTAACCTGGGAATTGCG	599
Qy	605	TTTGAATCTACAGGCTAGAGTGTGGGACAGGGAGTGGAAATTCGATGTAGAGCTGA	664
Db	600	TTTGAATCTACAGGCTAGAGTGTGGGACAGGGAGTGGAAATTCGATGTAGAGCTGA	659
Qy	665	ATGCGTAGAGATATGGAAGAAATCATGATGGCGAAGGACGCTCTGGGTTAACTGACG	724
Db	660	ATGCGTAGAGATATGGAAGAAATCATGATGGCGAAGGACGCTCTGGGTTAACTGACG	719
Qy	725	CTCATGCAAGAAAGGTGGGGAGCAAAACGATTAAGTATCCTCGGTATGCCAGCGCTTAA	784
Db	720	CTCATGCAAGAAAGGTGGGGAGCAAAACGATTAAGTATCCTCGGTATGCCAGCGCTTAA	779
Qy	785	ACGATGTCAACTAGTGTGTGGGCCCTTAATTAAGGCTTGTAAGCGAACCTAAACGGTGAATT	844
Db	780	ACGATGTCAACTAGTGTGTGGGCCCTTAATTAAGGCTTGTAAGCGAACCTAAACGGTGAATT	839
Qy	845	GACCGCCTGGGGAAGTACGGTCGCAAGATTAAAACTCAAGGAATTGACGGGACCCGCAC	904
Db	840	GACCGCCTGGGGAAGTACGGTCGCAAGATTAAAACTCAAGGAATTGACGGGACCCGCAC	899
Qy	905	AAGCGGTGATTAATGTGATTAAATTCGATGCAACGCGAAAACTTACCTAACCTTTGACA	964
Db	900	AAGCGGTGATTAATGTGATTAAATTCGATGCAACGCGAAAACTTACCTAACCTTTGACA	959
Qy	965	TGTAGCGAAATTTTCAAGATTAAGATTAGTGTGCGGAACGCTTAACAACAAGTGTGCAT	1023
Db	960	TGTAGCGAAATTTTCAAGATTAAGATTAGTGTGCGGAACGCTTAACAACAAGTGTGCAT	1019
Qy	1024	GCGTGTGCTCAGCTGTGTGCGAAGATGTTGGGTTAAATTCGCGCAACAGCGCAACCTT	1083
Db	1020	GCGTGTGCTCAGCTGTGTGCGAAGATGTTGGGTTAAATTCGCGCAACAGCGCAACCTT	1079
Qy	1084	GTCATTAATTCGCATCTTATAGTTGGGCACTTTAATGACACTGCGGATGACAAACCGGAG	1143
Db	1080	GTCATTAATTCGCATCTTATAGTTGGGCACTTTAATGACACTGCGGATGACAAACCGGAG	1139
Qy	1144	GAAAGTGGGGATGAAGTCAAGTCCATAGCCCTTAATGGGTTAAAGGCTTCAACGTAATAC	1203
Db	1140	GAAAGTGGGGATGAAGTCAAGTCCATAGCCCTTAATGGGTTAAAGGCTTCAACGTAATAC	1199

QY	1204	AATGGCGCGTACAGAGGGTTGGCCAAACCGGAGGGAGGCTTAATCTCAGAAAGGCGCTCG	1263
Db	1200	AATGGCCCGTACAGAGGGTTGCCAACCCGGAGGGGAGCTTAATCTCAGAAAGGCGCTCG	1259
QY	1264	TAGTCCGGATCGGAGTCTGCATCTCGACTCCGTGGAAGTCCGAATCGCTAGTAATCGCGGA	1323
Db	1260	TAGTCCCGGATCGGAGTCTGCATCTCGACTCCGTGGAAGTCCGAATCGCTAGTAATCGCGGA	1319
QY	1324	TCAGCATGTGCGCGGTGAATAGTTCCCGGGTCTTTGTACACCGGCCGTGACACCATATGGG	1383
Db	1320	TCAGCATGTGCGCGGTGAATAGTTCCCGGGTCTTTGTACACCGGCCGTGACACCATATGGG	1379
QY	1384	AGTGGGTTTCAACGAGAAAGCAGTAGTCTAACCGTAAAGAGCGGCGCTTGGCCACGGTGAAGAT	1443
Db	1380	AGTGGGTTTCAACGAGAAAGCAGTAGTCTAACCGTAAAGAGGCGGCGCTTGGCCACGGTGAAGAT	1439
QY	1444	TCATGA 1449	
Db	1440	TCATGA 1445	

RESULT 14	AF272420	1450 bp	DNA	linear	BCT 05-DEC-2000
LOCUS	AF272420	1450 bp	DNA	linear	BCT 05-DEC-2000
DEFINITION	Nitrosomonas aestuarii 16S ribosomal RNA gene, partial sequence.				
ACCESSION	AF272420				
VERSION	AF272420.1	GI:11545280			
KEYWORDS					
SOURCE					
ORGANISM	Nitrosomonas aestuarii				
REFERENCE	Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas.				
AUTHORS	1 (bases 1 to 1450)				
TITLE	Purkhold, U., Pommerening-Rose, A., Juretschko, S., Schmid, M.C., Koops, H.P. and Wagner, M.				
JOURNAL	Phylogeny of all recognized species of ammonia oxidizers based on comparative 16S rRNA and amoA sequence analysis: implications for molecular diversity surveys				
PUBMED	Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)				
REFERENCE	11097916				
AUTHORS	2 (bases 1 to 1450)				
TITLE	Purkhold, U., Pommerening-Rose, A., Juretschko, S., Schmid, M.C., Koops, H.P. and Wagner, M.				
JOURNAL	Direct Submission				
FEATURES	Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische Universitaet Muenchen, Am Hoechinger 4, Freising 85350, Germany				
SOURCE	Location/Qualifiers				
1. 1450					
/organism="Nitrosomonas aestuarii"					
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/db_xref="taxon:52441"					
<1_>1450					
/product="16S ribosomal RNA"					
ORIGIN					
Query Match	95.0%; Score 1383.6; DB 1; Length 1450;				
Best Local Similarity	97.6%; Pred. No. 1,2e-14;				
Matches 1415; Conservative	0; Mismatches 34; Indels 1; Gaps 1;				
QY	2 TTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGACGCGACGAGTCGTCGATC	61			
Db	1 TTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGACGCGACGAGTCGTCGATC	60			
QY	62 TGGGCGGAGTGGCGGACGGGTGAGTAATGCATCGGAAGTATCCGAAAGAGGGGGGTAA	121			
Db	61 TGGGCGGAGTGGCGGACGGGTGAGTAATGCATCGGAAGTATCCGAAAGAGGGGGGTAA	120			
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VERSION AF272424.1 GI:11545284
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REFERENCE
1 (bases 1 to 1513)
Purkhoid, U., Pommerening-Roser, A., Juretschko, S., Schmid, M.C.,
Koops, H.P. and Wagner, M.
Phylogeny of all recognized species of ammonia oxidizers based on
comparative 16S rRNA and amoA sequence analysis: implications for
molecular diversity surveys
Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
11057916
JOURNAL
PUBMED 2 (bases 1 to 1513)
REFERENCE
Purkhoid, U., Pommerening-Roser, A., Juretschko, S., Schmid, M.C.,
Koops, H.P. and Wagner, M.
Direct Submission
JOURNAL
Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische
Universitaet Muenchen, Am Hochanger 4, Freising 85350, Germany
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AUTHORS	Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.		
REFERENCE	1 (bases 1 to 1954)		
	Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan.D., Han,B., Zhang,Q. and Wang,S.		
TITLE	Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63		
JOURNAL	Plant J. 42 (5), 772-780 (2005)		
PUBMED	15918889		
COMMENT	Contact: Wang S National Key Laboratory of Crop Genetic Improvement Hauzhong Agricultural University Wuhan 430070, China Tel: 86-27-87282044 Fax: 86-27-87287092 Email: shiipingwang@hotmail.com Seq primer: T7. Location/Qualifiers		
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LOCUS

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genomic survey sequence.
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VERSION
B2439740.1 GI:26695676
KEYWORDS
GSS.
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ORGANISM
Brassica oleracea
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REFERENCE

1 (bases 1 to 1084)
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utecher, T.R., Wortman, J.R., White, O., and Town, C.D.

TITLE

Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis

JOURNAL

Genome Res. 15 (4): 487-495 (2005)

COMMENT

Other GSSs: BONDUS4TF
Contact: Chris Town
TIGR

FEATURES

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES

Location/Qualifiers
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DB 182 AAGAAAGGTTACGTAATTAATCGTCACTGACGATGATGCAAGAGAGACACCGGC 218
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QY 477 TAACTAGTCCAGCAGACCGCGGTAAATAGAGGTGCAAGCGTTAATCGAAATTAATCGG 536
    |||
DB 219 TAACTAGTCCAGCAGACCGCGGTAAATAGAGGTGCAAGCGTTAATCGAAATTAATCGG 278
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QY 537 GCGTAAAGGTCGCGAGGCGGCTTTGTAGTCAAGTGAATATCCCGGGCTTAACTGG 596
    |||
DB 279 GCGTAAAGGTCGTAAGTGTGCTTTTAAAGTCCGCGTCAAAATCCAGGCGTCAACCTTG 338
    |||

QY 597 GAATTCGTTTGAATCAAGAGCTAGAGTGTGACAGAGAGTGAATTCATGATGTA 656
    |||
DB 339 GACAGCGGTGAAATTAACAGCTTGAAGTACGTAAGGAGGAGGAATTTCCGGTGGG 398
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QY 657 GCAGTGAATGCGTGAATGAGAAAGAACATGATGCGGAAGGACCTCTCGGGTTAA 716
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Db      399 GCGGTGAAGATGCGTAGATGCGAAGAAACCAACGCGGAAGACACTCTGTGCGGCCGA 458
Qy      717 CACTGACGCTCATGACGAAAGCGTGGAGCAACAGATTAATACCTGTGTAGTCCA 776
Db      459 CACTGACACTGACGACGAAAGCTGAGGAGCGAATGGAATTAGATACCCCGAGTGTCT 518
Qy      777 GCGCCTAAAGATGCACTAGTGTGTGGGCTTATTAGGCTTG--GTAAAGAACCTAAC 834
Db      519 AGCGGTAAACGATGATCTAGGCGCTGTGCTATGACCGGTGACGCTGTACCTAAC 578
Qy      835 GCGTGAAGTTGACCGCTGGGAGTACCGTGCACAGATTAACCTCAAGAAATGACGG 894
Db      579 GCGTTAAGTATCCGCTCGGGAGTACGTTGCGAAGATGAACCTCAAGAAATGACGG 638
Qy      895 GGACCCCGCAAGCGCGGTGATTTATGTGATTAATGATGCAACCGCAAAAACCTTACT 954
Db      639 GGGCCCGCAAGCGGTGACATGTGTTAATGATGCAAAACGAAAGAACCTTAACA 698
Qy      955 ACCCTGACATGACGGAATTTCTAGAGATGATTAATG--CTTGGGGAAGCTTAACA 1013
Db      699 GGGCTGACATGCGCGGATCTCTTGAAGAGAGGGGTCTTGGGAACGCGACACA 758
Qy      1014 GGTGCTGATGAGCTGTCTGACGCTGCTGATGATGTTGGGTTAAGTCCGCAACGAG 1073
Db      759 GGTGCTGATGAGCTGTCTGACGCTGCTGATGATGTTGGGTTAAGTCCGCAACGAG 818
Qy      1074 CGCAACCTTGTCTATTAAATGCTCATTTGTTGGGCACTTTAATGACCTGCGGTGA 1133
Db      819 CGCAACCTTGTCTATTAAATGCTCATTTGTTGGGCACTTTAATGACCTGCGGTGA 878
Qy      1134 CAACCCGGAAGAGTGGGGAGTACGTCAAGTCCCTAATGAGGTTAAGGCTTCA 1193
Db      879 TAAACCGGAAGAGTGGGGAGTACGTCAAGTCCCTAATGAGGTTAAGGCTTCA 938
Qy      1194 CACGTAAATACATGCGCGGTACAGAGGGTTGCCAACCGCGAGGGAGCTAATCTCAGA 1253
Db      939 CACGTGCTACATGCGCGGTACAGAGGGTTGCCAACCGCGAGGGAGCTAATCTCAGA 998
Qy      1254 AAGGCGCTGATGTCGAGTGGAGTCTGCAACTGCACTCGTGAAGTCCGATGCTTAG 1313
Db      999 AACCCTGCTCAGTGGATGCAAGGCTGCAACTGCGCTGATGAAGCGGATGCTTAG 1058
Qy      1314 TAAATCGCGG 1322
Db      1059 TAAATCGCGG 1067

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LOCUS   CK296497 941 bp mRNA linear EST 02-AUG-2004
DEFINITION Nicotiana benthamiana mixed tissue cDNA library,
normalised, full-length Nicotiana benthamiana cDNA clone NEMD226 5'
end, mRNA sequence.
ACCESSION CK296497
VERSION   CK296497.1 GI:39881943
KEYWORDS EST.
SOURCE   Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 941)
Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A., Day, B.,
Stebkiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.

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/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMD226"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_id="Nicotiana benthamiana mixed tissue cDNA
library, normalised, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomat 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 43.8%; Score 637.8; DB 7; Length 941;
Best Local Similarity 81.3%; Pred. No. 1,8e-185;
Matches 752; Conservative 0; Mismatches 172; Indels 1; Gaps 1;

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78 CTGTGCGCAAGTGGCGGAGCGGTGATTAATGATCGGAAGCTAATCCGAAGAGGGGGTA 137
121 ACGCATGAAAGATGTCTAATACCGCATATCTCTAAGAGAGAAACAGAGGGAGTCAAA 180
138 ACGCTCGAAAGAGAGCGCTAATACCGCATACGCTTACCGGAGAAACAGAGGGAGCTTCG 197
181 GACCTTGGCTTTTGAAGCGCGCATGTCTGATTAAGTATGTTGGTGGGTAAAGCCTTAC 240
198 GACCTTGGCTTTTGAAGCGCGCATGTCTGATTAAGTATGTTGGTGGGTAAAGCCTTAC 257
241 CAAGCGACCATGATGTTGTTGTGAGAGAGCAACGACCACTGGAGCTGAGACAG 300
258 CAAGCGACCATGATGTTGTTGTGAGAGAGATGATGATCACTGGAACCTGAGACAG 317
301 GCCGAGACTCTTACGGAGGAGAGAGTGGGAAATTTTGAACAATGAGCGCAAGCCTGATC 360
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361 CAGCAATGCCCGCTGATGGAAGAGCGCTTCGGTTGTAAAGCTCTTTCAGTCAAGAGA 420
378 CAGCAATGCCCGCTGATGGAAGAGCGCTTCGGTTGTAAAGCTCTTTCAGTCAAGAGA 437
421 AAGGTTACGTTAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 480
438 AAGGTTACGTTAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 497
481 TAGTGGCAGAGCGCGGTAAATACGTAAGGTTGCAACGTTAATCGAATTAATCTAGGCGT 540
498 TCTGTGCGAGAGCGCGGTAAATACGTAAGGTTGCAACGTTAATCGAATTAATCTAGGCGT 557
541 AAGGTTGCGAGCGCGCTTTGTAAGTCAAGATGGAATCCCGGGCTTAACTTGAAGAT 600
558 AAGGCGCGGTAAGTGTGTTGTTAATGTAATGGAATCCCGGGCTCAACCTGGAAGAC 617
601 TCGCTTGAATCAATCAAGCTAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
618 TGCAATCAAAATCGCAAGCTAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
661 TGAATGCTAGATATGAGAGACATGATGCGAAGGACGCTCTGAGTTAAGACT 720

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Db	678	TGAATGGTGGATATATGAAAGAAACAACAGTGGGGAAGCGAACCACTGGACTGATCT	737
Qy	721	GACCTCTATGCACGAAAGCGTGGGGAGGAAACAGATTAGATACCTGGTGTGCCACGC	780
Db	738	GACACTGAGGTGCGAAACCGTGGGAGCAAAACAGATTAGTACCTGGTGTGCCACGC	797
Qy	781	CTAAACGATGTCACCTAGTTGTTGGGCTTATTAGGCTTGGTAAAGAACTTAACGCGTGA	840
Db	798	GTAACCGATGTCAACTACCGCTGGCG-AGCCTTGAGCTCTTAGTGGCAGCTAACCCATT	856
Qy	841	AGTGAACCGCTGGGGAAGTACGGTGCAAGATTAACTCAAGAAATTGACGGGGACC	900
Db	857	AGTTGACCGCTGGGGAAGTACGGCGCCAGGTTAAATCTCAATGAAATTGACGGGGGCC	916
Qy	901	GCACAAGCGGTGATATATGAGATT	925
Db	917	GCACAAGCGGTGAGCATGTGGTTT	941

RESULT 6					
BZ447500/c					
LOCUS	BZ447500	1053 bp	DNA	linear	GSS_13-DEC-2002
DEFINITION	BZ447500				
DESCRIPTION	BONKFR40TR_BO_1_6_2_KB_tot Brassica oleracea genomic clone BONKFR40,				
FEATURES	genomic survey sequence.				

ACCESSION	B2497500
VERSION	B2447500.1
KEYWORDS	GI:26712943
SOURCE	GSS.
ORGANISM	Brassica oleracea Brassica oleracea <i>Epilobota viridiflora</i> : Streptomyces <i>Epilobota viridiflora</i> : Tracheophyta:

REFERENCE
AUTHORS

1 (bases 1 to 1053)
Ayele, M., Haas, B. J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utecherack, T. R., Wortman, J. R., White, O. R. and Town, C. D.
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

TITLE	JOURNAL	PUBMED	COMMENT
Whole genome shotgun sequencing of <i>Brassica oleracea</i> and its application to gene discovery and annotation in <i>Arabidopsis</i>	Genome Res. 15 (4), 487-495 (2005)	15805490	Other_GSSs: BONKRF40TF

Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208

FEATURES
source
1
1053
location/Qualifiers

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/organism="Brassica oleracea"
/mol_type="genomic DNA"
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total DNA inserted into pHS1 using BstXI linkers"
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Best Local Similarity	77.2%	Pred. No. 4.9e-184		
Matches 831, Conservative	0	Mismatches 218	Indels 27	Gaps 4

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Db -	1052	GGCCTCGCCTGATTAGCTAGTGGGTGGGCAATGCTTACCAAGCCATATACATGAGC	993
Qy	260	TGATCTGAGAGACGACCCAGCACACTTGAGACATGGGCCCACTCTTACGGGAG	319
Db	992	TGATCCAGAGAGATATACGCCACATCTGGGACTGAGACATGGGCCCACTCTTACGGGAG	933

Qy	320	GCAGCAGTGGGAAATTTTGGACAAATGGGCGCAACCTGATCCAGCAATGCGCGTGAAGT	379
Db	932	GCAGCAGTGGGAAATTTCCG-CAAATGGCGCAAAAGCTGACCGAGCAATGCGCGTGGAGG	874
Qy	380	AAGAAGCCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAGAAAAGTTACGGTAATAAT	439
Db	873	TAGAAGCCTTACGGGTCCTGAATCTTTTCCAGAGAGA-----	833
Qy	440	CGTCACTCATGACGGTATCGACAGAAAGACCGGCTTAATCAGTCGACAGCGCGGG	499
Db	832	-----AGCAATGACGGTATCTGGGGAAATAGACATCGGCTTAATCTGTGCACACAGCGCGG	777
Qy	500	TAATACCTAAGGTCGACAGCGTTATCGGAATTACTGGGCGTAAAGCGTGCACAGCGGCT	559
Db	776	TAATACGAGATGCAAGCGTTATCCGAAATGATTTGGCGTAAAGCGTGTAGGTGGCT	717
Qy	560	TTGTAACTCAGATGTGAATATCCCGGGCTTAACTCGGGAATTTGGCTTTGAAACTTCAAG	619
Db	716	TTTTTAAGTCGCGCTCAATATCCAGGGCTCAACCTTGACACAGCGGTGAAAATCTACCAAG	657
Qy	620	CTAGAGTGTGGCAGAGGAGAGGTGGAATTTCAATGTGTAGCAGTGAATATCGTAGAGATATG	679
Db	656	CTTAGAGTACGTTAGGGGCAAGAGGAATTTCCGCTGGAGCGGCTGAATATCGTAGAGATCGG	597

QY	880	GAAGAAATATCATGCGCAAGGACACCTCTCTGGGTAACATCAGAGCTCAAGCAAGAGC	753
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Db	536	TAGGGAGGCGCAATGGAGTTAGATATCCCACTAGTACTTAGCCGTAAACGATGGATCTAGG	477
QY	800	TGTTGGGCTTTATTAAGGCTTG--GTAAAGAACTTAACGCGTGAAAGTTGACCGCTGGGGA	857
Db	476	CGCGTGTGATATCGAACCCCGTGCAGTGTCTGTAAGCTTAAGCGCTTAAGTATCCGCTGGGGA	417
QY	858	GTACCGGTGCGAAGTTTAAATCTCAAAAGAAATTGACGGGGAGCCGCGACAAAGCGGTGATT	917
Db	416	GTACGTTTCGAAAGATGAATCTCAAGGAATTGACGGGGGCCCGCACAAAGCGGTGAGCA	357
QY	918	TGTGGATTAAATTGAGTSCAACGCGAATAAACCCTTACCTTACATGTAGCGGAATTTT	977
Db	356	TGTGTTTAAATTCGATSCAAAGCGAAGAACTTTCACAGGCTTGACATGCCGCGAATCCT	297
QY	978	CTAGAGATTAATTATAGT--CTTCGGGAGCGCTAACACAGGTCTCATAGCGCTGTGACG	1033
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QY	1037	TCGTGTGTGATGATGTGTGGGTAAATGCCCGCAACGACGCAACCTTGTCTTAATTGCC	1096
Db	236	TCCTTCCCTTAAGGTGTTTGGTTAGTCTCCGTAAGAGAGCGAAACCTGTGTGTTTGGTCC	177

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BZ431523.1	1010 bp	ACGTCAGATGCTCTATGAGCCCTTATAGGTAGGGCTTCACAGTAATATCAATGAGCGGTAC	1211
BZ431523.1	1010 bp	ACGTCAAGTATCATATGCCCCCTTATGCCCTGGGCGACACACGTGTCAATATGGCCGGGACA	57
BZ431523.1	1010 bp	GAGGGTTGCCAACCCCGCGAGGGGAGAGCTAATCTTCAGAAAGCGCTCGTAGTCCGGA	1272
BZ431523.1	1010 bp	AAGGCTCGCGATCCAGAGAGGGTAGCTAATCTCCAAAAACCCGTCCTCAGTTCCGA	1

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

GSS.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1010)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utecherack,T.R., Wortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
15805490
Other GSSs: BOMND86TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source
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Location/Qualifiers
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Query Match 43.1%; Score 627.8; DB 9; Length 1010;
Best Local Similarity 77.9%; Pred. No. 2.3e-182;
Matches 805; Conservative 0; Mismatches 202; Indels 26; Gaps 3;

211 GATTAGTAGTGTGGTGAAGGCTTACCAAGGCGACATCACTAGTGTGTGAGAG 270
1010 GATTAGTAGTGTGGTGAAGGCTTACCAAGGCGACATCACTAGTGTGTGAGAG 951
271 GACGACCAAGGCTTGTGAGAGCGGCGGAGCTCTCTAGCGGAGGCGAGCTGGG 330
950 GATATATAGCCACCTGAGAGTGAACAGCGCCAGCTCTCTAGCGGAGGCGAGCTGGG 891
331 GAATTTTGAACATGGGCGGAGGCTTATCCAGCAATGCGGCGTGAAGAGGCGCTT 390
890 GAATTTTCCGAAATGGGCGGAGGCTTATCCAGCAATGCGGCGTGAAGAGGCGCTT 831
391 CGGGTTGTAAGCTCTTCACTGAGAGGAAAGGTTACGTAATATCGTCACTCAG 450
830 CGGGTCCGAACTCTTCCGAGAGAGA-----AGCAATG 794
451 ACGGATTCGAGAGAGAGGCGGCTTACCTAGTCCAGAGCGCGGCTAATAGTAGG 510
793 ACGGATTCGAGAGAGAGGCGGCTTACCTAGTCCAGAGCGCGGCTAATAGTAGG 734
511 GTGCAAGGCTTATCGAATTAATCTAGGCGGCTTAAAGGCGGCGGCTTGTAGTAG 570
733 ATGCAAGGCTTATCGAATTAATCTAGGCGGCTTAAAGGCGGCTTGTAGTAGCG 674
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631 CAGAGGAGGCTGGAATTCATGTGTAGAGAGGAAATGCGTGAAGTATGGAAGAACATCG 690
613 TAGGGGCGAGAGGAAATTCGCTGTAGAGGCGTGAAGTATGGAAGTATGGAAGAACATCG 554
691 ATGCGAAGGAGGCGCTTGGGCTTAACTAGCGCTACGCAAGGAGGCGGAGGAGCA 750

Db 553 ACGCGAAGAGACTCTGTGGCGGACGACAGTGAAGAGAGCAAGAAAGTAGGAGCGCA 494
Qy 751 ACAGATTAATATACCTGCTGATGCTGAGCGCTTAAAGATGCACTAGTGTGGCGCTT 810
Db 493 ATGGATTAATATACCTGCTGATGCTGAGCGCTTAAAGATGCACTAGTGTGGCGCTT 434
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Db 433 TCGACCGCTGAGAGCTGCTGAGTGAAGCTGAGTGAAGCTGCGCTGGGAGTACGCTCGCA 374
Qy 869 AGATTAATATACCTGCTGATGCTGAGCGGAGCGGACGAGCGGCTGATGATGATGAT 928
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Qy 929 TCGATGCAAGCGGAGAGAGCTTACCTGCTGATGCTGAGCGGAGCGGCTGATGATGAT 988
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Qy 1228 ACCCGGAGGCGG 1240
Db 13 TCCCGGAGGCGG 1

RESULT 8
BH705272
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BH705272 1079 bp DNA linear GSS 20-FEB-2002
BOMKA47TF BO 2.3 KB Brassica oleracea genomic clone BOMKA47,
genomic survey sequence.
BH705272
BH705272.1 GI:18787746
GSS.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1079)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utecherack,T.R., Wortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
15805490
Other GSSs: BOMKA47TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source
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Location/Qualifiers
/organism="Brassica oleracea"
/mol_type="genomic DNA"

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/strain="T01000DH3"
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genomic DNA inserted into pBOS1 using BstXI linkers

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ORIGIN
Query Match      42.7%; Score 622.2; DB 9; Length 1079;
Best Local Similarity 76.5%; Pred. No. 1.3e-180;
Matches 812; Conservative 0; Mismatches 223; Indels 26; Gaps 3,

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Oy	246	CGACGATCATGATGTTGGTCTGAGAGACGACCAAGCACTGGGACTGAGACACGGCCCA	305
Db	102	CGATGATCATGATGCTGGTCCGAGAGATGATACGACCACTGGGACTGAGACACGGCCCA	161
Oy	306	GACTCTTACGGGGAGGACAGAGGGGGAATTTTGCACAATAGGCGCAAGGCTATCCAGCA	365
Db	162	GACTCTTACGGGAGGACAGAGTGGGGAATTTTCCGCAATGGCGCAAGGCTTACCGAGCA	221
Oy	366	ATGCCGCGTGAAGTGAAGAAGCCCTTCGGGTGTGAAAGCTCTTTCAGTCGAGAGAAAAG	425
Db	222	ATGCCGCGTGAAGGTGAAGAAGCCCTACGGGTCTGAACTTCTTTCCAGAGAAAAG----	276
Oy	426	TTACGGTAAATATATCTGTGACTCATGACGGTATCGACAGAGAAAGACCGGCTTAACTAGT	485
Db	277	-----AGCATATCGGTATCTGGGAAATATAGCATCGCTTAACTCTGT	318
Oy	486	GCCAGACACCGCGGTATATCTGAGGGTGCACACGTTAATCGGAATTACTGGCGTAAAG	545
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Db	439	TGGAATCTTACCAAGCTTGATGATCGGTAGGGGCGAGAGGAATTTCCGGTGAACGGGTGAAG	498
Oy	666	TGCGTAGATATGGAAGACATCGATGCGGAAGCGCTCTGGGTAACTACATGACCG	725
Db	499	TGCGTAGATATCGAAGAAACAACCAACGCGGAAGACCTGTCTGGCGGACATGACAC	558
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Db	859	TGGCTGTGTCAGCTCGTCCGCTTAAGTCTTTGGGTTAACTCCGCAACAGAGCAACCTT	918
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DEFINITION	BZ426201 BONDZ28TF BO_1.6.2_KB_tot Brassica oleracea genomic clone BONDZ28, genomic survey sequence.
ACCESSION	BZ426201
VERSION	BZ426201.1
KEYWORDS	GI:26667713
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ORGANISM	Brassica oleracea Brassicaceae
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 1016)
AUTHORS	Ayalew,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utecherack,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
JOURNAL	PUBMED
COMMENT	15805490 Other_GSSs: BONDZ28TR

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FEATURES
    source
        TIGR
        9712 Medical Center Drive, Rockville, MD 20850, USA.
        Tel: 301-838-3523
        Fax: 301-838-0208
        Email: cdtowne@tigr.org
        DNA is from a doubled haploid provided by Tom Osborn.
        Seq primer: TF
        Class: sheared ends
        Location/Qualifiers
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Db	1015	GGCTCGGCTCTGATTACTAGTGGTAAAGCAATAGTTTACCAAGGCGATCATGATAC	956	
OY	260	TGCTCTAGAGAGACGACACGACCACTGGGACTGAGACA GGGCCACACTCTTACGGGAG	319	
Db	955	TGGTCGAGAGAGATGATCAACCACTCGGGACCTGAGACACAGGCCACAGACTCTTACGGGAG	896	
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440	CGTGA	CTCA	TGACGG	TATGACA	GAAGA	GAAGCA	CCGG	CTAA	CTA	CGTGC	CAAG	CGCCGG	499
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619	CTTGA	GTC	ACGTA	TGAGG	GCAG	AGG	GAATTT	CCG	TGGA	GGCGGT	GAATG	GTGA	AGT
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259	CTT	GA	AA	GA	AG	GG	GTG	CTT	CG	GA	AC	GTAA	CA
1037	TCG	TG	TCG	TG	TCG	TG	TCG	TG	TCG	TG	TCG	TG	TCG
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1097	ATC	ATT	TG	GTG	GG	CA	CTT	TA	TG	AG	CTG	CG	GTG
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1157	ACG	TAA	AG	TCT	CAT	AG	CG	CTT	AT	G	GG	CTT	CA
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TITLE	JOURNAL	PIUMED	COMMENT
Utterback, T.R., Mortman, J.R., White, O.R. and Town, C.D.	Whole genome shotgun sequencing of <i>Brassica oleracea</i> and its application to gene discovery and annotation in Arabidopsis	Genome Res. 15 (4), 487-495 (2005)	15805490
TIGR	Contact: Chris Town		
9712 Medical Center Drive, Rockville, MD 20850, USA.			
Tel: 301-838-3523			
Fax: 301-838-0208			
Email: cdtown@tigr.org			
DNA is from a doubled haploid provided by Tom Osborn.			
Seq primer: TP			
Class: sheared ends.			
Location/Qualifiers			
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Oy	607	TGAACTACAAAGGCTAGAGTGTGCGAGAGGAGGTGAAATTCATGTGTAGCAGTGAAT	6666
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 ACCESSION BZ463550
 VERSION BZ463550.1 GI:26749465
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1044)
 Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
 Utecherback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
 TITLE Whole genome shotgun sequencing of Brassica oleracea and its
 JOURNAL application to gene discovery and annotation in Arabidopsis
 PUBMED Genome Res. 15 (4), 487-495 (2005)
 15805490
 COMMENT Other GSSs: BOMK86TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers
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 VERSION BZ494182.1 GI:27004681
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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 1 (bases 1 to 1051)
 Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
 Utecherback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
 TITLE Whole genome shotgun sequencing of Brassica oleracea and its
 JOURNAL application to gene discovery and annotation in Arabidopsis
 PUBMED Genome Res. 15 (4), 487-495 (2005)
 15805490
 COMMENT Other GSSs: BOMHR54TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers
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Best Local Similarity 78.5%; Pred. No. 7.6e-178;
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QY 508 AGGGTGAAGCGTTAATCGAATTACTGGGGGTAAAGGGTCCGACGGCGCTTTGTAAGT
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DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5'
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ACCESSION CK280527
VERSION CK280527
KEYWORDS GI:39850196
SOURCE EST.
ORGANISM Nicotiana benthamiana

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REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST743250
Contact: Robin Buell
The Institute for Genomic Research
5712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-arrray@igf.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
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Location/Qualifiers

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challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

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ORIGIN

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Query Match      41.3%; Score 601.4; DB 7; Length 889;
Best Local Similarity 81.4%; Pred. No. 3.3e-174;
Matches 709; Conservative 0; Mismatches 161; Indels 1; Gaps 1;

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Oy 301 GCCCGACCTCTTACCGGAGAGCAGCATGAGGAGATTTTGGACATGAGGCGCAGCTGATC 360
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Db 378 CAGCATGCGCGGTGTGTAGAGAGAGGCTTCCGATTTGAAGCACTTTAAGTTGGAGAGA 437
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Oy 661 TGAATGTGCTAGATGTGAGAAATCATGATGTGAGAGGAGCGCTTCCCTGGGTTAACT 720
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Db 738 GACACTGAGTGTGCAAGAGCGTGGGAGCAAAACAGATTAAGATCCCTGGTATCCAGCC 797
Oy 781 CTAACCATGTCAATTAAGTTGGGCTTATTAAG-GCTTGTAACGAAAGCTTAAGCGGTG 839
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Db 858 AAGTTGACCGCGCTGGGAGTACGGCGCAG 888

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RESULT 15      884 bp  mRNA  linear  EST 02-AUG-2004
CK280528      EST743250 Nicotiana benthamiana mixed tissue cDNA library,
LOCUS         normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5',
DEFINITION    end, mRNA sequence.
ACCESSION     CK280528
VERSION       CK280528.1 GI:39850200
KEYWORDS      EST.
SOURCE        Nicotiana benthamiana
ORGANISM      Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE     1 (bases 1 to 884)
AUTHORS       Buell, C.R., Hart, A., Ziemann, V., Karimychewa, S.A., Day, B.,
              Steakiewicz, B., Jin, H. and Baker, B.
TITLE         Generation of EST sequences from Nicotiana benthamiana
JOURNAL       Unpublished (2003)
COMMENT       other ESTs: EST743249

```

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES
source
Location/Qualifiers
1..884
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMA117"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
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/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 41.0%; Score 597.4; DB 7; Length 884;
Best Local Similarity 81.3%; Pred. No. 5.7e-173;
Matches 705; Conservative 0; Mismatches 161; Indels 1; Gaps 1;

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Oy 61 CTGTGGGAGTGGCGGACGGGTGATGATGATCGAAGCTATCCAGAAAGGGGGTAA 120
Db 78 CTGTGGGAGTGGCGGACGGGTGATGATGATGATGATGATGATGATGATGATGAT 137
Oy 121 ACGCATGGAAGATGCTAATACCGCATATATCTTAGAGAGAAAGCAGGGATCGAAA 180
Db 138 ACGCTCGAAGAACGACGCTAATACCGCATATACGCTTACCGAGAAAGCAGGGACCTTGC 197
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Db 258 CAAGCGACGATGCTAGTGGTCTGAGAGATGATCACTGAGAACTGAGACAG 317
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Oy 361 CAGCAATCCCGCGTGTAGTGAAGAGGCTTCCGGTGTGAAGCTCTTTCAGTGAAGAGA 420
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Db 498 TCTGTGCAAGACGCGCGGTAAATACGAGGGTGCAGGCTTAACTGGAATTCTGGGGGT 557
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Qy      721 GAGCGTCATGCAAGAAAGCGTGGGAGCAACAGATTAGATACCTGTAGTCCAGCC 780
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Search completed: April 6, 2006, 23:14:00
 Job time : 6258 secs

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New Bacteria capable of oxidizing ammonia to nitrite, for preventing or alleviating the accumulation of ammonia in fresh water aquaria, seawater aquaria and waste water.

Claim 2; Page 5; 62pp; English.

The invention relates to 4 novel types of ammonia-oxidising bacteria (AOB) found in freshwater aquaria. The bacteria are able to oxidise ammonia to nitrite and are members of the ammonia-oxidising bacteria family of the beta subdivision of Proteobacteria. The 4 types of bacteria can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene

XX Hovanec TA;
 XX
 DR WPI; 2004-304936/28.
 XX
 PT New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment.
 XX
 PS Disclosure; Page 8-9; 98pp; English.
 XX
 CC This sequence represents a 16S rDNA sequence derived from an ammonia
 CC oxidising bacteria (AOB). This sequence may be used in a composition
 CC which comprises an isolated bacterial strain that oxidizes ammonia to
 CC nitrite. The composition may be used for alleviating or preventing the
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least
 CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.
 XX
 SQ Sequence 1457 BP; 378 A; 315 C; 456 G; 308 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1457; DB 12; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1081 CTTGTCTAATTTTCCCATCATTTTGGTTGGGCTTTTATAGAGACTGCGGCTGACAAACCG 1140
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 DB 1141 GAGGAGTGGGGATGACGTCAGTCTCATGCTCTCATGCTCTTATGGGTAGGCTTTCACACGTAA 1200
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 QY 1261 TCGTAGTCCGGATCGGAGTCTGCAACTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 1320
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 DB 1441 GATTCTAGCTGGGCTG 1457
 RESULT 3
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 ID ABA02417 standard; DNA; 1457 BP.
 XX
 AC ABA02417;
 XX
 DT 29-AUG-2003 (revised)
 DT 04-MAR-2002 (first entry)
 XX
 Type A1 ammonia-oxidising bacterium 16S rRNA gene sequence, R7clone187.
 Type A1; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
 ribosomal RNA; aquarium; aquaculture; waste water treatment;
 bioremediation; ds.
 OS Nitrosomonadales.
 XX
 PN WO200190312-A1.

XX PD 29-NOV-2001.
 XX PF 17-MAY-2001; 2001WO-US016265.
 XX PR 19-MAY-2000; 2000US-00573684.
 XX PA (AQUA-) AQUARIA INC.
 XX PI Hovanec TA, Burrell PC;
 XX DR WPI; 2002-075367/10.
 XX PT New bacteria capable of oxidizing ammonia to nitrite, for preventing or
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
 XX aquaria and waste water.
 PS Claim 2; Page 6; 62pp; English.
 CC The invention relates to 4 novel types of ammonia-oxidising bacteria
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise
 CC ammonia to nitrite and are members of the ammonia-oxidising bacteria
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clones) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidising bacteria of the invention,
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. The present sequence represents R7clone187,
 CC a 16S rRNA gene sequence from the type A1 ammonia-oxidising bacterium of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;
 Query Match 99.7%; Score 1452.2; DB 6; Length 1457;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATTGAACCTGGCGCATGCTTTACACATGCAAGTCGAACCGCAGCAGCGATGCTTCAT 60
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 DB 901 GCACAACGGTGGATTTGATGATTAATTCGATCAACGCGAAGAAACCTTACCTACCCCTT 960
 QY 961 GACATGTAGCGAAATTTCTAGAGATAGATTAGTCTTTGGGAAACGCTAAACACAGTGTG 1020
 DB 961 GACATGTAGCGAAATTTCTAGAGATAGATTAGTCTTTGGGAAACGCTAAACACAGTGTG 1020
 QY 1021 CATGGCTGTGTCAGCTCGTGTGATGATGTTGGGTAAAGTCCCGCAACGAGCGCAACC 1080
 DB 1021 CATGGCTGTGTCAGCTCGTGTGATGATGTTGGGTAAAGTCCCGCAACGAGCGCAACC 1080
 QY 1081 CTTGTCAATTAATTTGCCATCATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140
 DB 1081 CTTGTCAATTAATTTGCCATCATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140
 QY 1141 GAGGAAGGTGGGATGACGTCAGTCTCTATGCGCTTTATGGGTAGGGCTTTCAACGTA 1200
 DB 1141 GAGGAAGGTGGGATGACGTCAGTCTCTATGCGCTTTATGGGTAGGGCTTTCAACGTA 1200
 QY 1201 TACATGGCGGTACAGAGGTTGCGAACCGGCGGGGGAGCTAATCTCAGAAAGCGG 1260
 DB 1201 TACATGGCGGTACAGAGGTTGCGAACCGGCGGGGGAGCTAATCTCAGAAAGCGG 1260
 QY 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCGTGAAGTCGGAATCGCTAGTAATCGC 1320
 DB 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCGTGAAGTCGGAATCGCTAGTAATCGC 1320
 QY 1321 GGATCAGCATGTCCGGTGAATACGTTCCGGGTCTTTGTACACACCGCCCGTCAACCAT 1380
 DB 1321 GGATCAGCATGTCCGGTGAATACGTTCCGGGTCTTTGTACACACCGCCCGTCAACCAT 1380
 QY 1381 GGGAGTGGGTTTACCAAGAGCAGGTAGTCTAACCGTTAAGAGGGGGCTTGGCAGCGTGA 1440
 DB 1381 GGGAGTGGGTTTACCAAGAGCAGGTAGTCTAACCGTTAAGAGGGGGCTTGGCAGCGTGA 1440
 QY 1441 GATTTCAGCTGGGGTG 1457
 DB 1441 GATTTCAGCTGGGGTG 1457

ID ADM32705 standard; DNA; 1457 BP.
 XX AC ADM32705;
 XX ET 17-JUN-2004 (first entry)
 XX DE AOB Type A1 R7clone187 16S rDNA.
 XX KW 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
 XX KW aqueous environment; freshwater; seawater; aquarium; ss.
 XX OS Nitrosomonas sp.
 XX PN W02004026772-A2.
 XX PD 01-APR-2004.
 XX PF 10-SEP-2003; 2003WO-US028210.
 XX PR 19-SEP-2002; 2002US-0386217P.
 XX PR 19-SEP-2002; 2002US-0386218P.
 XX PR 19-SEP-2002; 2002US-0386219P.
 XX PA (AQUA-) AQUARIA INC.
 XX PI Hovanec TA;
 XX DR WPI; 2004-304936/28.
 XX PT New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment.
 XX PS Disclosure; Page 10; 98pp; English.
 XX CC This sequence represents a 16S rDNA sequence derived from an ammonia
 CC oxidising bacteria (AOB). This sequence may be used in a composition
 CC which comprises an isolated bacterial strain that oxidizes ammonia to
 CC nitrite. The composition may be used for alleviating or preventing the
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least
 CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.
 XX SQ Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;
 Query Match 99.7%; Score 1452.2; DB 12; Length 1457;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATTGAACGCTGGCGCATGCTTTTACACATGCAAGTCGAACGCGCAGCAGGATGCTTGCAT 60
 DB 1 ATTGAACGCTGGCGCATGCTTTTACACATGCAAGTCGAACGCGCAGCAGGATGCTTGCAT 60
 QY 61 CTGTGGCGAGTGGCGGACGGGTGAGTAAATGCAATCGGAACGTATCCAGAGAGGGGTA 120
 DB 61 CTGTGGCGAGTGGCGGACGGGTGAGTAAATGCAATCGGAACGTATCCAGAGAGGGGTA 120
 QY 121 ACGCATCGAAGATGTGCTAATACCGCATATCTTAAGGAGGAAAGCAGGGGATCGAAA 180
 DB 121 ACGCATCGAAGATGTGCTAATACCGCATATCTTAAGGAGGAAAGCAGGGGATCGAAA 180
 QY 181 GACCTTGGCTTTTGGAGCGGCGGATGCTGATTAGCTAGTTGGTGGGGTAAAGCCCTAC 240
 DB 181 GACCTTGGCTTTTGGAGCGGCGGATGCTGATTAGCTAGTTGGTGGGGTAAAGCCCTAC 240
 QY 241 CAAGCGGACGATCAGTAGTGTGCTGAGAGGACGACCGACACCTGGGACTGAGACAG 300
 DB 241 CAAGCGGACGATCAGTAGTGTGCTGAGAGGACGACCGACACCTGGGACTGAGACAG 300
 QY 301 GCCCAGACTCTACGGGAGGAGCGAGTGGGNAATTTTGGCAATGGGCGCAAGCCTGATC 360
 DB 301 GCCCAGACTCTACGGGAGGAGCGAGTGGGNAATTTTGGCAATGGGCGCAAGCCTGATC 360

DB 301 GCCCAGACTCTACGGGAGGAGCGAGTGGGNAATTTTGGCAATGGGCGCAAGCCTGATC 360
 QY 361 CAGCAATGCCGCGTGAAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTTTCAGTCGAGAAGA 420
 DB 361 CAGCAATGCCGCGTGAAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTTTCAGTCGAGAAGA 420
 QY 421 AAAGGTTACGGTAAATTAATCGTGAATCATGACGCTATCGACAGAGGAGCACCAGCTAAC 480
 DB 421 AAAGGTTACGGTAAATTAATCGTGAATCATGACGCTATCGACAGAGGAGCACCAGCTAAC 480
 QY 481 TACGTGCCAGCAGCCGCGTAATACGTAGGTCAAGCGTTTAATCGGAATTTACTGGGCGT 540
 DB 481 TACGTGCCAGCAGCCGCGTAATACGTAGGTCAAGCGTTTAATCGGAATTTACTGGGCGT 540
 QY 541 AAAGGTTGCCAGCGCGCTTTTGAAGTCAGATGTAATCCCGGGCTTAACCTGGGAAT 600
 DB 541 AAAGGTTGCCAGCGCGCTTTTGAAGTCAGATGTAATCCCGGGCTTAACCTGGGAAT 600
 QY 601 TCGGTTTGAAGTCAACAGGCTTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 660
 DB 601 TCGGTTTGAAGTCAACAGGCTTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 660
 QY 661 TGAATCGGTAGAGATATGGAAGAACATCGATGCGAAGGAGCAGCTCTCTGGTTAAACACT 720
 DB 661 TGAATCGGTAGAGATATGGAAGAACATCGATGCGAAGGAGCAGCTCTCTGGTTAAACACT 720
 QY 721 GACGCTCATGCAAGAGCGTGGGAGCAACACAGGATTAGATACCTGGTGTAGTCCACGCC 780
 DB 721 GACGCTCATGCAAGAGCGTGGGAGCAACACAGGATTAGATACCTGGTGTAGTCCACGCC 780
 QY 781 CTAACGATGTCACACTAGTTGTTGGGCTTATAGGCTTGGTAAACGAGCTAAACGCGTGA 840
 DB 781 CTAACGATGTCACACTAGTTGTTGGGCTTATAGGCTTGGTAAACGAGCTAAACGCGTGA 840
 QY 841 AGTTGACCGCTGGGAGTACGCTGCGCAAGATTAAAACTCAAAGGAATTTGACGGGACCC 900
 DB 841 AGTTGACCGCTGGGAGTACGCTGCGCAAGATTAAAACTCAAAGGAATTTGACGGGACCC 900
 QY 901 GCACAGCGGTGGATTATGGAATTAATTCATGCAACGCGGAAAAAACCCTTACCTTACCCTT 960
 DB 901 GCACAGCGGTGGATTATGGAATTAATTCATGCAACGCGGAAAAAACCCTTACCTTACCCTT 960
 QY 961 GACATGTAGCGAAATTTTCTAGAGATAGATAGTCTCTGGGAACGCTAAACACAGTGTGTG 1020
 DB 961 GACATGTAGCGAAATTTTCTAGAGATAGATAGTCTCTGGGAACGCTAAACACAGTGTGTG 1020
 QY 1021 CATGGCTGTCTCAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080
 DB 1021 CATGGCTGTCTCAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080
 QY 1081 CTTGTCAATTAATTGGCATCAATTTGGTTGGGCACTTTTAATGAGACTGCGGTTGACAAACCG 1140
 DB 1081 CTTGTCAATTAATTGGCATCAATTTGGTTGGGCACTTTTAATGAGACTGCGGTTGACAAACCG 1140
 QY 1141 GAGGAAGTGGGATGAGTCAAGTCTCTATGGCCCTTATGGGTAGGGCTTTACACGTAA 1200
 DB 1141 GAGGAAGTGGGATGAGTCAAGTCTCTATGGCCCTTATGGGTAGGGCTTTACACGTAA 1200
 QY 1201 TACAATGGCGGTACAGAGGGTTGCAACCCCGGAGGGGAGCTAATCTCAGAAAGCGCG 1260
 DB 1201 TACAATGGCGGTACAGAGGGTTGCAACCCCGGAGGGGAGCTAATCTCAGAAAGCGCG 1260
 QY 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCCGTAAGTCGGAATCGCTAGTAATCGC 1320
 DB 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCCGTAAGTCGGAATCGCTAGTAATCGC 1320
 QY 1321 GGATCAGCATGTCGCGTGAATACGTTCCCGGGTCTTGTACACACCGCCCTCACACCAT 1380
 DB 1321 GGATCAGCATGTCGCGTGAATACGTTCCCGGGTCTTGTACACACCGCCCTCACACCAT 1380
 QY 1381 GGGAGTGGGTTTACCAAGAGCAGGTAGTCTAAACCGTAAAGAGGGGCGCTTGGCCACGGTGA 1440
 DB 1381 GGGAGTGGGTTTACCAAGAGCAGGTAGTCTAAACCGTAAAGAGGGGCGCTTGGCCACGGTGA 1440

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QY 1441 GATTCATGACTGGGTG 1457
DB 1441 GATTCATGACTGGGTG 1457

RESULT 5
ADM32723
ID ADM32723 standard; DNA; 1491 BP.
XX
AC ADM32723;
XX
DT 17-JUN-2004 (first entry)
XX
DE AOB BF16clone57 16S rDNA.
XX
KW 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS Nitrosomonas aestuarii.
XX
PN WO2004026772-A2.
XX
PD 01-APR-2004.
XX
PF 10-SEP-2003; 2003WO-US028210.
XX
PR 19-SEP-2002; 2002US-0386217P.
PR 19-SEP-2002; 2002US-0386218P.
PR 19-SEP-2002; 2002US-0386219P.
XX
PA (AQUA-) AQUARIA INC.
XX
PI Hovanec TA;
XX
DR WPI; 2004-304936/28.
XX
PT New composition comprising an isolated bacterial strain that oxidizes
PT ammonia to nitrite, useful for alleviating or preventing the accumulation
PT of ammonia in aqueous environment.
XX
PS Claim 1; Page 15; 98pp; English.
XX
CC This sequence represents a 16S rDNA sequence derived from an ammonia
CC oxidising bacteria (AOB). This sequence may be used in a composition
CC which comprises an isolated bacterial strain that oxidizes ammonia to
CC nitrite. The composition may be used for alleviating or preventing the
CC accumulation of ammonia in a medium. The ammonia is reduced by at least
CC 30% when compared with a level of ammonia that would exist in the absence
CC of the bacterial strain. The composition is useful for alleviating or
CC preventing the accumulation of ammonia in aqueous environment, e.g. a
CC freshwater or seawater aquarium.
XX
SQ Sequence 1491 BP; 392 A; 323 C; 457 G; 319 T; 0 U; 0 Other;

Query Match 95.5%; Score 1391.6; DB 12; Length 1491;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCAGCGATGCTTGCAT 60
DB 18 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCAGCGATGCTTGCAC 77
QY 61 CTGTGGCGAGTGGCGGACGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 78 CTGTGGCGAGTGGCGGACGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 137
QY 121 ACGCATCCAAAGATGCTGCTAATACCGCATATATCTTAAGGAGGAAGCAGGCGGATCGAAA 180
DB 138 ACGCATCCAAAGATGCTGCTAATACCGCATATATCTTAAGGAGGAAGCAGGCGGATCGAAA 197
QY 181 GACCTTGGCGCTTTTGGAGCGGCCGATGCTGATTAAGCTAGTGTGGTGGGTAAGGCGCTTAC 240

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DB 198 GACCTTGTGCTTTTGGAGCGGCCGATGCCTGATTAGCTAGTTGGTGGGTAAAGSCCTTAC 257
QY 241 CAAGCGACGATCAGTAGTTGGTCTGAGAGACACCAAGCCACACTGGGACTGAGACAGC 300
DB 258 CAAGGCAACGATCAGTAGTTGGTCTGAGAGACACCAAGCCACACTGGGACTGAGACAGC 317
QY 301 GCCCAGACTCCTCAGGAGGAGCAGCAGTGGGAAATTTTGGACAAATGGGCGCAAGCCTGATC 360
DB 318 GCCCAGACTCCTCAGGAGGAGCAGCAGTGGGAAATTTTGGACAAATGGGCGCAAGCCTGATC 377
QY 361 CAGCAATGCCCGGTGAGTGAAGAGGCTTCGGGTGTAAAGCTCTTTTCAGTCGAGAAAGA 420
DB 378 CAGCAATGCCCGGTGAGTGAAGAGGCTTCGGGTGTAAAGCTCTTTTCAGTCGAGAAAGA 437
QY 421 AAAGGTTACGCTAAATATCTGACTCATGACGCTATCGACAGAGAGACACCGCTAAC 480
DB 438 AAAGGTTGCTAAATATCTGACTCATGACGCTATCGACAGAGAGACACCGCTAAC 497
QY 481 TACGTGCAGCAGCGCGGTAAATACGTAGGTCGAAGCGTTAAATCGGAATTTTACCTGGGCGT 540
DB 498 TACGTGCAGCAGCGCGGTAAATACGTAGGTCGAAGCGTTAAATCGGAATTTTACCTGGGCGT 557
QY 541 AAAGGTCGCGCAGCGCGCTTTGTAAGTCAGATGAGTGAATTCGCCGGCTTAACTGGGGAAT 600
DB 558 AAAGGTCGCGCAGCGCGCTTTGTAAGTCAGATGAGTGAATTCGCCGGCTTAACTGGGGAAT 617
QY 601 TGGCTTTGAAACTACAAGGCTAGAGTGTGCGAGAGGAGGTGGAAATTCATGTGTAGCAG 660
DB 618 TGGCTTTGAAACTACAAGGCTAGAGTGTGCGAGAGGAGGTGGAAATTCATGTGTAGCAG 677
QY 661 TGAATCGTAGAGATATGGAAGAACATCGATGTCGAGAGGAGCGCTCCTGCGGTAAACACT 720
DB 678 TGAATCGTAGAGATATGGAAGAACATCGATGTCGAGAGGAGCGCTCCTGCGGTAAACACT 737
QY 721 GACGCTCATGCAGAAAGCGTGGGAGCAAAACAGAGTTAGATACCTCGTGTAGTCCACGCC 780
DB 738 GACGCTCATGCAGAAAGCGTGGGAGCAAAACAGAGTTAGATACCTCGTGTAGTCCACGCC 797
QY 781 CTAAACGATGCTCAACTAGTTGTTGGGCTTACCTAGGCTTGGTAAACGCTGTAACCGCTGA 840
DB 798 CTAAACGATGCTCAACTAGTTGTTGGGCTTACCTAGGCTTGGTAAACGCTGTAACCGCTGA 857
QY 841 AGTTGACCGCTGCGGAGTAGTACGCTCGCAAGATTAAAACTCAAAGGAATTCAGCGGAGCCC 900
DB 858 AGTTGACCGCTGCGGAGTAGTACGCTCGCAAGATTAAAACTCAAAGGAATTCAGCGGAGCCC 917
QY 901 GCACAAGCGGTGGATTTATGATGATTAATTCGATGCAACGCGGAAAAACCTTACCTACCCCT 960
DB 918 GCACAAGCGGTGGATTTATGATGATTAATTCGATGCAACGCGGAAAAACCTTACCTACCCCT 977
QY 961 GACATGTAGCGAAATTTTCTAGAGATAGATTAGTG-CITTCGGGAACGCTTAACACAGGTGCT 1019
DB 978 GACATGTAGCGAAATTTTCTAGAGATAGATTAGTG-CITTCGGGAACGCTTAACACAGGTGCT 1037
QY 1020 GCATGGCTGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
DB 1038 GCATGGCTGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097
QY 1080 CTTTGTCAATTAATTCGATCAATTTGTTGGGCACTTTAAATGAGACTGCGCGGTGCAAAACC 1139
DB 1098 CTTTGTCAATTAATTCGATCAATTTGTTGGGCACTTTAAATGAGACTGCGCGGTGCAAAACC 1157
QY 1140 GGAGGAGGTGGGAGTACGCTCAAGTCTCATGCGCTTATGGGTAGGCTTTCACAGTA 1199
DB 1158 GGAGGAGGTGGGAGTACGCTCAAGTCTCATGCGCTTATGGGTAGGCTTTCACAGTA 1217
QY 1200 ATACAATGGGCGGTACAGAGGGTTGCCAAACCGCGAGGGGGAGCTAATCTCAGAAAAGCGC 1259
DB 1218 ATACAATGGGCGGTACAGAGGGTTGCCAAACCGCGAGGGGGAGCTAATCTCAGAAAAGCGC 1277
QY 1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGCTGGAATCGGTAATCGTAGTAATCG 1319
DB 1278 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGCTGGAATCGGTAATCGTAGTAATCG 1337

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DY 1320 CGGATCAGATGTCGGCGTGATACGTTCCCGGTCCTTTGTACACACCGCGGTACACCA 1379
 Db 1338 CGGATCAGATGTCGGCGTGATACGTTCCCGGTCCTTTGTACACACCGCGGTACACCA 1397
 DY 1380 TGGGAGTGGGTTTACACAGAGCAGGTAGTCTTAACCGTAAAGAGGGCGCTTGGCCACGGTG 1439
 Db 1398 TGGGAGTGGGTTTACACAGAGCAGGTAGTCTTAACCGTAAAGAGGGCGCTTGGCCACGGTG 1457
 DY 1440 AGATTATGACTGGGGTG 1457
 Db 1458 AGATTATGACTGGGGTG 1475
 RESULT 6
 ADM32722
 ID ADM32722 standard; DNA; 1494 BP.
 XX
 AC ADM32722;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE AOB P4clone31 16S rDNA.
 XX
 KW 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
 KW aqueous environment; freshwater; seawater; aquarium; ss.
 XX
 OS Nitrosomonas aestuarii.
 XX
 PN W02004026772-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 10-SEP-2003; 2003WO-US028210.
 XX
 PR 19-SEP-2002; 2002US-0386217P.
 PR 19-SEP-2002; 2002US-0386218P.
 PR 19-SEP-2002; 2002US-0386219P.
 XX
 PA (AQUA-) AQUARIA INC.
 XX
 PI Hovanec TA;
 XX
 XX WPI; 2004-304936/28.
 DR
 XX
 PT New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment.
 XX
 PS Claim 1; Page 14; 98pp; English.
 CC
 CC This sequence represents a 16S rDNA sequence derived from an ammonia
 CC oxidizing bacteria (AOB). This sequence may be used in a composition
 CC which comprises an isolated bacterial strain that oxidizes ammonia to
 CC nitrite. The composition may be used for alleviating or preventing the
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least
 CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.
 XX
 SQ Sequence 1494 BP; 392 A; 327 C; 459 G; 316 T; 0 U; 0 Other;
 Query Match 93.3%; Score 1359.2; DB 12; Length 1494;
 Best Local Similarity 96.3%; Pred. No. 0;
 Matches 1402; Conservative 0; Mismatches 53; Indels 1; Gaps 1;
 QY 1 ATTGAACGCTGGCGGATGCTTTACATGCAAGTCGAACGGGACGAGATGTTGCAT 60
 Db 19 ATTGAACGCTGGCGGATGCTTTACATGCAAGTCGAACGGGACGAGATGTTGCAT 78
 QY 61 CTGTGGCGAGTGGCGGATGAGTAAATGATCGGAACTATCCAGACAGGGGGTA 120

Db 79 CTGTGGCGAGTGGCGGAGTGAATATGATCGGAACTGTCTCCGAAAGTGGGGATA 138
 QY 121 ACGCATCGAAAGATGTCTTAATACCGCATATATCTCTAAGAGGAAAGCAGGGGATCGAAA 180
 Db 139 ACGCATCGAAAGATGTCTTAATACCGCATATATCTCTAAGAGGAAAGCAGGGGATCGAAA 198
 QY 181 GACCTCGCGCTTTTGGAGCGCGCATGTCTGATTAGCTAGTTGGTGGGTAAGGSCCTTAC 240
 Db 199 GACCTTGTCTTTTGGAGCGCGCATGCTGATTAGCTAGTTGGTGGGTAAGGSCCTTAC 258
 QY 241 CAAGCGCAGCATCAGTATGTTGGTCTGAGAGGACACACGACCACTGGGACTGAGACACG 300
 Db 259 CAAGGCAACGATCAGTATGTTGGTCTGAGAGGACACACGACCACTGGGACTGAGACACG 318
 QY 301 GCCCAGACTCTCTACGGGAGGACGAGTGGGGAATTTTGGCAATTTGGGCGCAAGCCTGATC 360
 Db 319 GCCCAGACTCTCTACGGGAGGACGAGTGGGGAATTTTGGCAATTTGGGCGCAAGCCTGATC 378
 QY 361 CAGCAATGCCCGGTGAGTGAAGAGGCTTTCGGGTTCTAAAGCTCTTTTCACTCAGAGAAGA 420
 Db 379 CAGCAATGCCCGGTGAGTGAAGAGGCTTTCGGGTTCTAAAGCTCTTTTCACTCAGAGAAGA 438
 QY 421 AAAGGTTACGGTAAATATCTGATCATGACGCTATCGACAGAAAGCAACCGGCTAAC 480
 Db 439 AAAGGTTGACTTAATTAATCACAACTTTATGACGCTACCGACAGAAAGCAACCGGCTAAC 498
 QY 481 TAGTGCCACGACGCGCGTAAATACGTAGGTCGACGCTTAATCGGAATTTACTTGGGCGT 540
 Db 499 TAGTGCCACGACGCGCGTAAATACGTAGGTCGACGCTTAATCGGAATTTACTTGGGCGT 558
 QY 541 AAAGGTTGCCGCGCGCTTTTGAAGTCAGATGTGAATCCCGGGCTTAACTTGGGAAT 600
 Db 559 AAAGGTTGCCGCGCGCTTTTGAAGTCAGATGTGAATCCCGGGCTTAACTTGGGAAT 618
 QY 601 TGGCTTTGAAACTACAGGCTAGAGTGTGCGAGGAGGTGGAATTCATGTGTAGCAG 660
 Db 619 TGGCTTTGAAACTACAGGCTAGAGTGTGCGAGGAGGTGGAATTCATGTGTAGCAG 678
 QY 661 TGAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGAGCGCTCTTGGGTTAACT 720
 Db 679 TGAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGAGCGCTCTTGGGTTAACT 738
 QY 721 GAGCTCATGCGAAGCGTGGGAGCAACAGGATTAGATACCTTGGTAGTCCAGGCC 780
 Db 739 GAGCTCATGCGAAGCGTGGGAGCAACAGGATTAGATACCTTGGTAGTCCAGGCC 798
 QY 781 CTAAACGATGTCAACTAGTGTGTTGGGCTTTATTAGGCTTGTAACTGAAAGCTAACCGCTGA 840
 Db 799 CTAAACGATGTCAACTAGTGTGTTGGGCTTTATTAGGCTTGTAACTGAAAGCTAACCGCTGA 858
 QY 841 AGTTGACCGCTGGGAGTACGGTCCGAAGATTAAACTCAAGGAATTTGACGGGAGCCC 900
 Db 859 AGTTGACCGCTGGGAGTACGGTCCGAAGATTAAACTCAAGGAATTTGACGGGAGCCC 918
 QY 901 GCACAGCGGTGATTTATGGAATTAATTCGATCGAAGCGGAAACCTTACCTACCCCTT 960
 Db 919 GCACAGCGGTGATTTATGGAATTAATTCGATCGAAGCGGAAACCTTACCTACCCCTT 978
 QY 961 GACATGTAGCGAAATTTTCTAGAGATAGATTAGTG-CTTCGGGAAACGCTAACACAGGTGCT 1019
 Db 979 GACATGTAGCGAAATTTTCTAGAGATAGATTAGTG-CTTCGGGAAACGCTAACACAGGTGCT 1038
 QY 1020 GCATGGTGTGTCAGCTCGTGTGAGATGTTGGTAAAGTCCCGCAACGAGCGCAAC 1079
 Db 1039 GCATGGTGTGTCAGCTCGTGTGAGATGTTGGTAAAGTCCCGCAACGAGCGCAAC 1098
 QY 1080 CCTTGTCAATTAATTTGGCATCATTTTGGTGGGCACTTTAATGAGACTCCCGGTGCAAAACC 1139
 Db 1099 CCTTGTCAATTAATTTGGCATCATTTTGGTGGGCACTTTAATGAGACTCCCGGTGCAAAACC 1158
 QY 1140 GGAGGAAGGTGGGGAATGACGTCAGTCCCTCATGCCCTTATGGGTAGGGCTTACACGTA 1199
 Db 1159 GGAGGAAGGTGGGGAATGACGTCAGTCCCTCATGCCCTTATGGGTAGGGCTTACACGTA 1218

QY 1200 ATCAATGCGGTACAGAGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGCGC 1259
 DB 1219 ATCAATGCGGTACAGAGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGCGC 1278
 QY 1260 GTCTAGTCGGATCGGATCTGCAACTCGACTCCGCTGAAGTCGGAATCGCTAGTAATCG 1319
 DB 1279 GTCTAGTCGGATCGGATCTGCAACTCGACTCCGCTGAAGTCGGAATCGCTAGTAATCG 1338
 QY 1320 CCGATCAGCATGTCCGGTGAATAGTTCCCGGCTTTGTACACACCGCGCTGACACA 1379
 DB 1339 CCGATCAGCATGTCCGGTGAATAGTTCCCGGCTTTGTACACACCGCGCTGACACA 1398
 QY 1380 TGGGAGTGGTTTACCAAGCAGGTAGTCTAACCGTAAGGAGGCGCTTGCCACGGTG 1439
 DB 1399 TGGAGTTGGCTGCACCAAGTAGTGTCTAACCCCTCGGAGGACGCTTACCACGGTG 1458
 QY 1440 AGATTCAATGACTGGG 1455
 DB 1459 TGGTCAATGACTGGG 1474

RESULT 7

ADM32721
 ID ADM32721 standard; DNA; 1467 BP.

XX ADM32721;

DT 17-JUN-2004 (first entry)

XX AOB P4clone42 16S rDNA.

XX 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;
 KW aqueous environment; freshwater; seawater; aquarium; ss.

XX Nitrosomonas aestuarii.

OS WO2004026772-A2.

PN 01-APR-2004.

PD 10-SEP-2003; 2003WO-US028210.

PF 19-SEP-2002; 2002US-0386217P.

PR 19-SEP-2002; 2002US-0386218P.

PR 19-SEP-2002; 2002US-0386219P.

XX (AQUA-) AQUARIA INC.

XX Hovanec TA;

XX WPI; 2004-304936/28.

XX New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment.

PS Claim 1; Page 13; 98pp; English.

XX This sequence represents a 16S rDNA sequence derived from an ammonia
 CC oxidizing bacteria (AOB). This sequence may be used in a composition
 CC which comprises an isolated bacterial strain that oxidizes ammonia to
 CC nitrite. The composition may be used for alleviating or preventing the
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least
 CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.

XX Sequence 1467 BP; 384 A; 320 C; 451 G; 312 T; 0 U; 0 Other;

Query Match 93.3%; Score 1358.8; DB 12; Length 1467;

Best Local Similarity 97.2%; Pred. No. 0;

Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;
 QY 1 ATTGAACGCTGGCGCATGCTTTACATGCAAGTCGAACCGCGAGCTGCTTGCAT 60
 DB 16 ATTGAACGCTGGCGCATGCTTTACATGCAAGTCGAACCGCGAGCTGCTTGCAT 75
 QY 61 CTGTGGCGAGTGGCGAGCGGTGAGTAATCATCGGAACGCTATCCAGAACAGGGGGTA 120
 DB 76 CTGTGGCGAGTGGCGAGCGGTGAGTAATCATCGGAACGCTATCCAGAACAGGGGGTA 135
 QY 121 ACGCATCGAAAGATGTCTAATACCGCATATATCTTAAGGAGGAAAGCAGGGGATCGAAA 180
 DB 136 ACGCATCGAAAGATGTCTAATACCGCATATATCTTAAGGAGGAAAGCAGGGGATCGAAA 195
 QY 181 GACCTTGGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTGTGGGTAAAGSCCTAC 240
 DB 196 GACCTTGGCTTTTGGAGCGGCCGATGTCTGATTAGCTAGTGTGGGTAAAGSCCTAC 255
 QY 241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACACCGACCATCTGGGACTTGAGACACG 300
 DB 256 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACACCGACCATCTGGGACTTGAGACACG 315
 QY 301 GCCCAGACTCTCTACCGGAGGCGAGTCAGTGGGAAATTTTGGACAATGGGCGAAGCCTGATC 360
 DB 316 GCCCAGACTCTCTACCGGAGGCGAGTCAGTGGGAAATTTTGGACAATGGGCGAAGCCTGATC 375
 QY 361 CAGCAATGCCCGGTGAGTGAAGAGCGCTTCGGGTGTGAAGCTCTTTCACTCGAAGAAGA 420
 DB 376 CAGCAATGCCCGGTGAGTGAAGAGCGCTTCGGGTGTGAAGCTCTTTCACTCGAAGAAGA 434
 QY 421 AAGGTTACGCTAATTAATCGTCACTCATGACGCTATCGACAGAGGAGACCGGCTAAC 480
 DB 435 AAGGTTACGCTAATTAATCAAACTTATGATGTACGACAGAGGAGACCGGCTAAC 494
 QY 481 TACGTGCCAGCAGCGCGGTAATACGTAGGTGCAAGCGTTAAATCGGAATTAATCTGGGCGT 540
 DB 495 TACGTGCCAGCAGCGCGGTAATACGTAGGTGCAAGCGTTAAATCGGAATTAATCTGGGCGT 554
 QY 541 AAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTAATCCCGGGCTTAACCTGGGAAAT 600
 DB 555 AAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTAATCCCGGGCTTAACCTGGGAAAT 614
 QY 601 TGGCTTTGAAACTACAAGGCTTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 660
 DB 615 TGGCTTTGAAACTACAAGCTAGAGTGTAGCAGAGGAGGTGGAATTCATGTGTAGCAG 674
 QY 661 TGAATCGGTAGAGATATGGAAGAACATCGATGCGAAGGCGAGCTCTCTGGTTAAACACT 720
 DB 675 TGAATCGGTAGAGATATGGAAGAACATCGATGCGAAGGCGAGCTCTCTGGTTAAACACT 734
 QY 721 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGTACCTGTGTAGTCCAGCC 780
 DB 735 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGTACCTGTGTAGTCCAGCC 794
 QY 781 CTAAACGATGTCAACTAGTTGTTGGGCTTATTAAGGCTTGTGTAACGAAGCTTAAACGCTGA 840
 DB 795 CTAAACGATGTCAACTAGTTGTTGGGCTTATTAAGGCTTGTGTAACGAAGCTTAAACGCTGA 854
 QY 841 AGTTGACCGCTGGGAGTACGCTCGCAAGATTAATACTCAAAGGAATTCGCGGGAGCC 900
 DB 855 AGTTGACCGCTGGGAGTACGCTCGCAAGATTAATACTCAAAGGAATTCGCGGGAGCC 914
 QY 901 GCACAGCGGTGATTAATGATGGAATTAATTCATGCAACCGGAGGAAACCTTACCTACCCCT 960
 DB 915 GCACAGCGGTGATTAATGATGGAATTAATTCATGCAACCGGAGGAAACCTTACCTACCCCT 974
 QY 961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAACGCTTAAACACAGGTGCT 1019
 DB 975 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGCCTTCGGGAACGCTTAAACACAGGTGCT 1034
 QY 1020 GCATGGCTGTCGTCAGCTCGTGTGAGATGTTGGTGTAAAGTCCCGCAACGAGCGCAAC 1079
 DB 1035 GCATGGCTGTCGTCAGCTCGTGTGAGATGTTGGTGTAAAGTCCCGCAACGAGCGCAAC 1094

QY 1080 CCTGTGATTAATGCGATCAATTTGGTGGGCACTTTTAATGAGACTGCCGGTGACAAACC 1139
DB |||||
QY 1095 CCTGTGATTAATGCGATCAATTTGGTGGGCACTTTTAATGAGACTGCCGGTGACAAACC 1154
DB |||||
QY 1140 GGAGGAAGGTGGGGATGACGTCAGTCAAGTCTCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1199
DB |||||
QY 1200 ATCAATGCGCGCTACAGAGGGTTGCCAACCCCGGAGGGGAGCTTAATTCAGAAAGCGC 1259
DB |||||
QY 1215 ATCAATGCGCGCTACAGAGGGTTGCCAACCCCGGAGGGGAGCTTAATTCAGAAAGCGC 1274
DB |||||
QY 1260 GTCGTAGTCCGATCGAGTCTCAACTCGACTCCGTGAAGTCCGAATCGTAGTAATCG 1319
DB |||||
QY 1275 GTCGTAGTCCGATCGAGTCTCAACTCGACTCCGTGAAGTCCGAATCGTAGTAATCG 1334
DB |||||
QY 1320 CGGATCAGCATGTCGGGGTGAATACGTTCCCGGGTCTTTGTACACACCGCCGCTCACACCA 1379
DB |||||
QY 1335 CGGATCAGCATGTCGGGGTGAATACGTTCCCGGGTCTTTGTACACACCGCCGCTCACACCA 1394
DB |||||
QY 1380 TGGGAGTGGGTTTCCACAGAGCAGGAGTGTCTTAACCGTAAAGGAGGGCGCTTGCACGGTG 1439
DB |||||
QY 1395 TGGGAGTGGGTTTCCACAGAGCAGGAGTGTCTTAACCGTAAAGGAGGGCGCTTGCACGGTG 1453
DB |||||
QY 1440 AGATTTCATCACTGG 1453
DB |||||
QY 1454 AGATTTCATCACTGG 1467
DB |||||

RESULT 8

ABR02418
ID ABA02418 standard; DNA; 1458 BP.

XX
AC ABA02418;

XX
DT 29-AUG-2003 (revised)
DT 04-MAR-2002 (first entry)

XX Type B ammonia-oxidising bacterium 16S rRNA gene sequence, R3clone5.

XX Type B; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
KW ribosomal RNA; aquarium; aquaculture; waste water treatment;
KW bioremediation, ds.

XX Nitrosomonadales.

OS WO200190312-A1.

XX 29-NOV-2001.

XX 17-MAY-2001; 2001WO-US016265.

XX 19-MAY-2000; 2000US-00573684.

XX (AQUA-) AQUARIA INC.

XX Hovanec TA, Burrell PC;

XX WPI; 2002-075367/10.

XX New bacteria capable of oxidizing ammonia to nitrite, for preventing or
PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
PT aquaria and waste water.

XX Claim 2; Page 7; 62pp; English.

XX The invention relates to 4 novel types of ammonia-oxidising bacteria
CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise
CC ammonia to nitrite and are members of the ammonia-oxidising bacteria
CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
CC sequences (ABR02416-ABR02419), and are classified as AOB type A (e.g.,

CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
CC gene sequences of the ammonia-oxidising bacteria of the invention,
CC oligonucleotide probes and primers for the detection of these bacteria,
CC and compositions comprising the bacteria. The bacteria of the invention
CC are useful in biological filters for reducing ammonia accumulation in
CC both freshwater and seawater aquaria. They may also be used in waste
CC water treatment and in bioremediation processes to reduce the level of
CC pollution caused by ammonia. The present sequence represents R3clone5, a
CC 16S rRNA gene sequence from the type B ammonia-oxidising bacterium of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX

SQ Sequence 1458 BP; 368 A; 342 C; 466 G; 282 T; 0 U; 0 Other;

Query Match 88.4%; Score 1287.6; DB 6; Length 1458;

Best Local Similarity 93.6%; Pred. No. 0;

Matches 1366; Conservative 0; Mismatches 89; Indels 5; Gaps 2;

QY 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCCAGCACGATGCTTGCAT 60

DB |||||

QY 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCCAGCACGATGCTTGCAT 58

DB |||||

QY 61 CTGCTGGCGAGTGGCGGACGGGTGATTAATGCATCGGAACGTATCCAGAAGAGGGGGTA 120

DB |||||

QY 59 CTGCTGGCGAGTGGCGGACGGGTGATTAATGCATCGGAACGTATCTTCGAGGGGGGATA 118

DB |||||

QY 121 ACGCATCGAAAGATGTGCTTAATACCGCATATCTCTAAGGAGGAAGCAGGGGATCGAAA 180

DB |||||

QY 119 ACGCACCGAAAGGTGTCTTAATACCGCATATCTCTAAGGAGGAAGCAGGGGATCGCAA 178

DB |||||

QY 181 GACCTTGGCGCTTTTGGAGCGCGCGATGCTGTATAGTAGTTGGTGGGGTAAAGGCGCTAC 240

DB |||||

QY 179 GACCTTGGCGCTTTTGGAGCGCGCGATGCTGTATAGTAGTTGGTGGGGTAAAGGCGCTAC 238

DB |||||

QY 241 CAAGCGGACGATCAGTAGTTGGTCTGAGAGGACGACACCACTGGGACTGAGACACG 300

DB |||||

QY 239 CAAGCGGACGATCAGTAGTTGGTCTGAGAGGACGACACCACTGGGACTGAGACACG 298

DB |||||

QY 301 GCCGAGACTCTACGGGAGGCGAGCTGGGGAATTTGGACAAATGGGCGCAAGCTGATC 360

DB |||||

QY 299 GCCGAGACTCTCTACGGGAGGCGAGCTGGGGAATTTGGACAAATGGGCGCAAGCTGATC 358

DB |||||

QY 361 CAGCAATCCCGCTGAGTGAAGAGCGCTTCCGGTGTAAAGCTCTTTCAGTCCGAGAACG 420

DB |||||

QY 359 CAGCCATCCCGCTGAGTGAAGAGCGCTTCCGGTGTAAAGCTCTTTCAGTCCGAGAACG 418

DB |||||

QY 421 AAAGGTTACGGTAAATATCGTGACTCATGACGGTATCGACAGAGAAGCACCGGCTAAC 480

DB |||||

QY 419 AACGGTCACGGCTAATACCCGGTACTACTGACGGTACCGGAAGAAGACACCGGCTAAC 478

DB |||||

QY 481 TACGTGCCAGCAGCGCGGTAATAGTAGGGTGCAGCGGTTAATCGGAATTAATCGGGCGT 540

DB |||||

QY 479 TACGTGCCAGCAGCGCGGTAATAGTAGGGTGCAGCGGTTAATCGGAATTAATCGGGCGT 538

DB |||||

QY 541 AAAGGTTGCAGCGCGGCTTTTGAAGTCAGATGTAAATCCCGGGCTTAACTCGGAAT 600

DB |||||

QY 539 AAAGGTTGCAGCGCGGCTTTTGAAGTCAGATGTAAATCCCGGGCTTAACTCGGAAT 598

DB |||||

QY 601 TCGGTTTCAAACTACAAGGCTAGAGTGTGGCAGAGGGAGGTGGAATTCATGTAGTAGAG 660

DB |||||

QY 599 TCGGTTTCAAACTACAAGGCTAGAGTGTGGCAGAGGGAGGTGGAATTCATGTAGTAGAG 658

DB |||||

QY 661 TGAATGCTAGAGATATGGAAGACATCGATGGCGAGGAGCGCTCTCGGGTTAACTACT 720

DB |||||

QY 659 TGAATGCTAGAGATATGGAAGACATCGATGGCGAGGAGCGCTCTCGGGTTAACTACT 718

DB |||||

QY 721 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGATTTAGATACCTGTGTAGTCCACGCC 780

DB |||||

QY 719 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGATTTAGATACCTGTGTAGTCCACGCC 778

DB |||||

QY 781 CTAAACGATGCAACTAGTGTGGGCGCTTATTAGGCTTGGTAAACGAAAGCTAACCGTGA 840

DB |||||

QY 779 CTAAACGATGCAACTAGTGTGGGCGCTTATTAGGCTTGGTAAACGAAAGCTAACCGTGA 838

DB |||||

QY 841 AGTTGACCGCTCGGAGTACGCTCGAAGATTAAACTCAAGGAATTGACGGGACCC 900
 Db |||||
 QY 839 AGTTGCGCGCTCGGAGTACGCTCGAAGATTAAACTCAAGGAATTGACGGGACCC 998
 Db |||||
 QY 901 GCACAAAGCGGTGATTATGTGGATTAAATTCGATGCAACGCGAAACCTTTACCTACCTTT 960
 Db |||||
 QY 899 GCACAAAGCGGTGATTATGTGGATTAAATTCGATGCAACGCGAAACCTTTACCTACCTTT 958
 Db |||||
 QY 961 GACATGTAGCGAATTTCTAGAGATGATTAGTGC---TTCGGGAACGCTTAACACAGGTG 1017
 Db |||||
 QY 959 GACATGTAGCGAAGCGCGGAGAGGTGGGTGCGCGAAAGGAGCGGTAAACACAGGTG 1018
 Db |||||
 QY 1018 CTCGATGGCTGCTCGATGCTGCTGATGATGTTGGTAAATGCTCCGCAACGCGCA 1077
 Db |||||
 QY 1019 CTCGATGGCTGCTCGATGCTGCTGATGATGTTGGTAAATGCTCCGCAACGCGCA 1078
 Db |||||
 QY 1078 ACCCTTGTCATTAAATGCGCATCAATTTGGTTGGGCACCTTTAATGAGACTGCGCGTGACAAA 1137
 Db |||||
 QY 1079 ACCCTTGTCATTAAATGCGCATCAATTTGGTTGGGCACCTTTAATGAGACTGCGCGTGACAAA 1138
 Db |||||
 QY 1138 CCGGAGGAAGGTGGGATGATGATGCTCAAGTCTCATGCGCCTTATGGTAGGGCTTACACG 1197
 Db |||||
 QY 1139 CCGGAGGAAGGTGGGATGATGATGCTCAAGTCTCATGCGCCTTATGGTAGGGCTTACACG 1198
 Db |||||
 QY 1198 TAATACAATGGCGGTACAGAGGGTTGCCAACCGCGGGGGAGCTAATCTCAGAAAGC 1257
 Db |||||
 QY 1199 TAATACAATGGCGGTACAGAGGGTTGCCAACCGCGGGGGAGCTAATCTCAGAAAGC 1258
 Db |||||
 QY 1258 GCGTCTAGTCCGGATCGGAGTCTGCAACTCGCACTCGCTGAACTCGGAATCGCTAGTAAT 1317
 Db |||||
 QY 1259 GCGTCTAGTCCGGATCGGAGTCTGCAACTCGCACTCGCTGAACTCGGAATCGCTAGTAAT 1318
 Db |||||
 QY 1318 CCGCGATCAGCATGTCGCGGTGAATAGCTTCCCGGTCTTTGATACACACCGCGCGTCACAC 1377
 Db |||||
 QY 1319 CCGCGATCAGCATGTCGCGGTGAATAGCTTCCCGGTCTTTGATACACACCGCGCGTCACAC 1378
 Db |||||
 QY 1378 CATGGAGTGGGTTTCCACAGAGCAGGTAGTCTAACCGTTAGGAGGCGCTTGCACGG 1437
 Db |||||
 QY 1379 CATGGAGTGGGTTTCCACAGAGCAGGTAGTCTAACCGTTAGGAGGCGCTTGCACCG 1438
 Db |||||
 QY 1438 TGAGATTCTAGTGGGGTG 1457
 Db |||||
 QY 1439 TGAGATTCTAGTGGGGTG 1458
 Db |||||

RESULT 9
 ADM32706
 ID ADM32706 standard; DNA; 1458 BP.
 XX ADM32706;
 AC
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE AOB Type B R3clones 16S rDNA.
 XX
 KW 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
 KW aqueous environment; freshwater; seawater; aquarium; SS.
 XX Nitrosomonas sp.
 XX WO2004026772-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 10-SEP-2003; 2003WO-US028210.
 XX
 PR 19-SEP-2002; 2002US-0386217P.
 PR 19-SEP-2002; 2002US-0386218P.
 PR 19-SEP-2002; 2002US-0386219P.
 XX
 PA (AQUA-) AQUARIA INC.
 XX

PI Hovanec TA;
 XX WPI; 2004-304936/28.
 DR
 XX
 PT New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment..
 PT
 XX Disclosure; Page 11; 98pp; English.
 PS
 XX
 CC This sequence represents a 16S rDNA sequence derived from an ammonia
 CC oxidising bacteria (AOB). This sequence may be used in a composition
 CC which comprises an isolated bacterial strain that oxidizes ammonia to
 CC nitrite. The composition may be used for alleviating or preventing the
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least
 CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.
 XX
 SQ Sequence 1458 BP; 368 A; 342 C; 466 G; 282 T; 0 U; 0 Other;
 Query Match 88.4%; Score 1287.6; DB 12; Length 1458;
 Best Local Similarity 93.6%; Pred. No. 0;
 Matches 1366; Conservative 0; Mismatches 89; Indels 5; Gaps 2;
 QY 1 ATTGAACGCTCGCGCATGCTTTACATGCAAGTTCGAACGCGACGCGATGCTTGCAAT 60
 Db |||||
 QY 1 ATTGAACGCTCGCGCATGCTTTACATGCAAGTTCGAACGCGACGCGCGCAACC-- 58
 Db |||||
 QY 61 CTGTGGCGAGTGGCGGACGGGTGATGTAATGATCGGAACGCTATCCAGAAAGAGGGGGTA 120
 Db |||||
 QY 59 CTGTGGCGAGTGGCGGACGGGTGATGTAATGATCGGAACGCTATCTTCGAGGGGGGATA 118
 Db |||||
 QY 121 ACGCATCGAAAGATGTGCTAATACCGCATATCTTAAGAGAGGAAGCAGGGGATCGAAA 180
 Db |||||
 QY 119 ACGCACCAGAAAGGTGTGCTAATACCGCATATCTTCAGGAGAAAGCAGGGGATCGCAA 178
 Db |||||
 QY 181 GACCTGGCTTTTGGAGCGCGGATGCTGATAGCTAGTGTGGGTAAAGGCTTAC 240
 Db |||||
 QY 179 GACCTGGCTTTTGGAGCGCGGATGCTGATAGCTAGTGTGGGTAAAGGCTTAC 238
 Db |||||
 QY 241 CAAGCGACGATCAGTATGCTGAGAGGACGACGACCACTGGGACTGAGACACG 300
 Db |||||
 QY 239 CAAGCGACGATCAGTATGCTGAGAGGACGACGACCACTGGGACTGAGACACG 298
 Db |||||
 QY 301 GCCCAGACTCTTACGGGAGGCGACGATGGGGAAATTTTGGACAATGGGCGCAAGCTGATC 360
 Db |||||
 QY 299 GCCCAGACTCTTACGGGAGGCGACGATGGGGAAATTTTGGACAATGGGCGCAAGCTGATC 358
 Db |||||
 QY 361 CAGCAATGCGCGGTGAGTGAAGAGGCTTCGGGTGTAAGGCTTTTCAGTTCGAGAGA 420
 Db |||||
 QY 359 CAGCAATGCGCGGTGAGTGAAGAGGCTTCGGGTGTAAGGCTTTTCAGTTCGAGAGA 418
 Db |||||
 QY 421 AAAGGTTACGGTAAATAATCGTGACTCATGACGGTATCGACAGAAAGACCGGCTAAC 480
 Db |||||
 QY 419 AACGGTCAAGCTAATACCGGTGACTGACGGTACCGGAGAGAGAGCACCAGCTAAC 478
 Db |||||
 QY 481 TACGTGCCAGCAGCGCGGTAAATACGATAGGTGCAAGCGTTAATCGGAATTTACTGGGGGT 540
 Db |||||
 QY 479 TACGTGCCAGCAGCGCGGTAAATACGATAGGTGCAAGCGTTAATCGGAATTTACTGGGGGT 538
 Db |||||
 QY 541 AAAGGTTGCGCAGCGGCTTTGTAAGTCAAGATGTAATCCCGGCTTTAACCTGGGAAT 600
 Db |||||
 QY 539 AAAGGTTGCGCAGCGGCTTTGTAAGTCAAGATGTAATCCCGGCTTTAACCTGGGAAT 598
 Db |||||
 QY 601 TCGGTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 660
 Db |||||
 QY 599 TCGGTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 658
 Db |||||
 QY 661 TGAATCGTATAGATATGGAAGAACATCGATGCGGAAGCAGCGCTCTCTGGGTTAACACT 720
 Db |||||
 QY 659 TGAATCGTATAGATATGGAAGAACATCGATGCGGAAGCAGCGCTCTCTGGGTTAACACT 718
 Db |||||

QY 721 GACGCTCATGCACGAAGCGTGGGAGCAAA CAGGATTAGATACCTCGTAGTCCACGCC 780
 DB 719 GACGCTCAGGCGACGAAGCGTGGGAGCAAA CAGGATTAGATACCTCGTAGTCCACGCC 778
 QY 781 CTAAACGATGTCACTAGTGTGGGCTTATTAGGCTTGGTAAACGAAGCTAACGGCTCA 840
 DB 779 CTAAACGATGTCACTAGTGTGGGCTTATTAGGCTTGGTAAACGAAGCTAACGGCTCA 838
 QY 841 AGTTGACCCGCTGGGAGTACGGTCCGAAGATTAAAACTCAAAGGAATTGACGGGACCC 900
 DB 839 AGTTGGCCGCTGGGAGTACGGTCCGAAGATTAAAACTCAAAGGAATTGACGGGACCC 898
 QY 901 GCACAGCCGCTGATTTATGTTGATTAATTCGATGCAACCGGAACCTTACTACCTT 960
 DB 899 GCACAGCCGCTGATTTATGTTGATTAATTCGATGCAACCGGAACCTTACTACCTT 958
 QY 961 GACATGTAGCGAATTTCTAGAGATAGATTAGTGC---TTCCGGGAACGCTAACACAGGTG 1017
 DB 959 GACATGTAGCGAAGCCCGGAGAGGTGGTGTGCCGAAGAGGAGCGGTAAACAGGTG 1018
 QY 1018 CTGCATGGCTGTCTGAGCTCGTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCA 1077
 DB 1019 CTGCATGGCTGTCTGAGCTCGTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCA 1078
 QY 1078 ACCTTGTCAATTAATTCGCAATTTGGTTGGGCACTTTAATGAGACTCCCGTGACAAA 1137
 DB 1079 ACCTTGTCAATTAATTCGCAATTTGGTTGGGCACTTTAATGAGACTCCCGTGACAAA 1138
 QY 1138 CCGGAGGAGGTGGGATGACGCTCAAGTCTCATGCGCCCTTATGGTAGGGCTTCACAG 1197
 DB 1139 CCGGAGGAGGTGGGATGACGCTCAAGTCTCATGCGCCCTTATGGTAGGGCTTCACAG 1198
 QY 1198 TAATACAAATGGGCGTACAGAGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGC 1257
 DB 1199 TAATACAAATGGGCGTACAGAGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGC 1258
 QY 1258 GCGTGTAGTCCGGATCGGAGTCTGCAACTCGACTCGGTGAAGTCGGAATCGTAGTAAT 1317
 DB 1259 GCGTGTAGTCCGGATCGGAGTCTGCAACTCGACTCGGTGAAGTCGGAATCGTAGTAAT 1318
 QY 1318 CCGGATCAGCATGTCCGGTGAATACGTTCCCGGTCTTGATACACCCGCCCGTACAC 1377
 DB 1319 CCGGATCAGCATGTCCGGTGAATACGTTCCCGGTCTTGATACACCCGCCCGTACAC 1378
 QY 1378 CATGGAGTGGGTTTCCACAGAGCAGGTAGTCTAAACCGTAAAGGAGGCGCTTGCCACGG 1437
 DB 1379 CATGGAGTGGGTTTCCACAGAGCAGGTAGTCTAAACCGTAAAGGAGGCGCTTGCCACGG 1438
 QY 1438 TGAGATTCAATGACTGGGGTG 1457
 DB 1439 TGAGATTCAATGACTGGGGTG 1458

RESULT 10
 ABA02419
 ID ABA02419 standard; DNA; 1460 BP.
 XX ABA02419;
 AC ABA02419;
 XX ABA02419;
 DT 29-AUG-2003 (revised)
 DT 04-MAR-2002 (first entry)
 XX
 DE Type C ammonia-oxidising bacterium 16S rRNA gene sequence, R3clone47.
 XX Type C; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
 KW ribosomal RNA; aquarium; aquaculture; waste water treatment;
 KW bioremediation; ds.
 XX Nitrosomonadales.
 OS
 XX WO200190312-A1.
 PN
 XX

PD 29-NOV-2001.
 XX 17-MAY-2001; 2001WO-US016265.
 XX 19-MAY-2000; 2000US-00573694.
 XX (AQUA-) AQUARIA INC.
 XX Hovanec TA, Burrell PC;
 PI MPI; 2002-075367/10.
 DR
 XX
 XX New bacteria capable of oxidizing ammonia to nitrite, for preventing or
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
 PT aquaria and waste water.
 XX
 PS Claim 2; Page 8; 62pp; English.
 XX The invention relates to 4 novel types of ammonia-oxidising bacteria
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise
 CC ammonia to nitrite and are members of the ammonia-oxidising bacteria
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidising bacteria of the invention,
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. The present sequence represents R3clone47, a
 CC 16S rRNA gene sequence from the type C ammonia-oxidising bacterium of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 1460 BP; 388 A; 316 C; 454 G; 302 T; 0 U; 0 Other;

Query Match 84.4%; Score 1230.2; DB 6; Length 1460;
 Best Local Similarity 92.3%; Pred. No. 0;
 Matches 1351; Conservative 0; Mismatches 103; Indels 9; Gaps 5;
 QY 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCAGCGATGCTTGCAT 60
 DB 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAG--CGGGGCTTCGCG 58
 QY 61 CTGCTGGCGAGTGGCGGAGTGAATGATCGATCGGAACGTTATCCAGAAAGGCGGGTA 120
 DB 59 CTGCGCGGAGTGGCGGAGTGAATGATCGATCGGAACGTTATCCCTTAAGTGGGGAATA 118
 QY 121 ACGCATCGAAAGATGTGCTAATACCGCATATATCTTAAGGAGGAAGCAGGGGATCGAAA 180
 DB 119 ACGCATCGAAAGATGTGCTAATACCGCATAT-CTCTGAGGAGAAAGCAGGGGATCGCAA 177
 QY 181 GACCTTGGCTTTTGGAGCGCGCATGCTGATTAGTGTAGTGGGTAAAGGCTTAC 240
 DB 178 GACCTTGGCTTAAAGGAGCGCGCATGCTGATTAGTGTAGTGGGTAAAGGCTTAC 237
 QY 241 CAAGGCGACGATCAGTAGTGTGCTTGAGAGGACGACGACCACTCTGGGACTGAGACAG 300
 DB 238 CAAGGCGACGATCAGTAGTGTGCTTGAGAGGACGACCACTCTGGGACTGAGACAG 297
 QY 301 GCCGAGACTCTTACCGGAGGCGAGTGGGGAATTTTGGCAATGGGCGCAAGCTGATC 360
 DB 298 GCCGAGACTCTTACCGGAGGCGAGTGGGGAATTTTGGCAATGGGCGCAAGCTGATC 357
 QY 361 CAGCAATCCCGCTCAGTGAAGAGGCGCTTCGGGTGTAAAGCTCTTTTCACTCGAAGAA 420
 DB 358 CAGCAATCCCGCTCAGTGAAGAGGCGCTTCGGGTGTAGAGCTCTTTTGTAGTCAAGAA 417
 QY 421 AAAGGTTACGGTAAATTAATCGTGAATCGAGCGGTATCGACAGAAAGACACCGGCTAAC 480
 DB 418 AAGATCATGATGATTAATTAATGATTTATGACGGTACTGACAGAAAGACACCGGCTAAC 477

QY 481 TAGCTGCCAGCCGCGGTAATACGTAGGTCGAAGCGTTAATCGAATTACTGGCGT 540
 Db 478 TAGCTGCCAGCCGCGGTAATACGTAGGTCGAAGCGTTAATCGAATTACTGGCGT 537
 QY 541 AAAGGGTGGCGAGCGGCTTTGTAAGTACAGTGTGAATCCCGGGCTTAACCTGGGAAT 600
 Db 538 AAAGGGTGGCGAGCGGCTTTGTAAGTACAGTGTGAATCCCGGGCTTAACCTGGGAAT 597
 QY 601 TGGCTTTGAACTACAAAGCTAGAGTGTGGCAGAGGAGGTGAATTCATGTGTAGCAG 660
 Db 598 TGGCTTTGAACTACAAAGCTAGAGTGTGGCAGAGGAGGTGAATTCATGTGTAGCAG 657
 QY 661 TGAATGCGGTAGAGATATGAAGAATCATCGATGCGAAGGAGCGCTTCTGGGTACACT 720
 Db 658 TGAATGCGGTAGAGATATGAAGAATCATCGATGCGAAGGAGCGCTTCTGGGTACACT 717
 QY 721 GACGCTCATGCACAAAGCGTGGGAGCAAAAGGATTAAGATACCTGTGTAGTCCACGCC 780
 Db 718 GACGCTCATGCACAAAGCGTGGGAGCAAAAGGATTAAGATACCTGTGTAGTCCACGCC 777
 QY 781 CTAACGATGTCAACTAGTTGTTGGGCTTATTA--GGCTTGTGTAAGAGCTAACGCGT 838
 Db 778 CTAACGATGTCAACTAGTTGTTGGGCTTATTA--GGCTTGTGTAAGAGCTAACGCGT 837
 QY 839 GAGTTGACCGCTGGGAGTACGTCGCAAGATTAAGATCAAGGAATTCAGCGGGAC 898
 Db 838 GAGTTGACCGCTGGGAGTACGTCGCAAGATTAAGATCAAGGAATTCAGCGGGAC 897
 QY 899 CCGCACAGCGGTGATTTAGTGGATTAATTCATGCAAGCGCAAAACCTTACCTACCC 958
 Db 898 CCGCACAGCGGTGATTTAGTGGATTAATTCATGCAAGCGCAAAACCTTACCTACCC 957
 QY 959 TTGACATGATGAGGAATTTCTAGAGATAGATTAGTGC---TTGCGAAACGCTAACACAGG 1015
 Db 958 TTGACATGATGAGGAATTTCTAGAGATAGATTAGTGC---TTGCGAAACGCTAACACAGG 1017
 QY 1016 TGTGTCATGCTGCTGACGTCGTCGAGATGTTGGTAACTCCCGCAACGAGCG 1075
 Db 1018 TGTGTCATGCTGCTGACGTCGTCGAGATGTTGGTAACTCCCGCAACGAGCG 1077
 QY 1076 CAACCTTGTCAATTAATGTCATCATT-TGGTTGGGCACTTTAATGAGACTGCGGCTGAC 1134
 Db 1078 CAACCTTGTCAATTAATGTCATCATT-TGGTTGGGCACTTTAATGAGACTGCGGCTGAC 1137
 QY 1135 AAACCGGAGAGGTGGGATGACGTCAGTCTCATGCGCCCTTATGGGTAGGGCTTAC 1194
 Db 1138 AAACCGGAGAGGTGGGATGACGTCAGTCTCATGCGCCCTTATGGGTAGGGCTTAC 1197
 QY 1195 ACCTAATACAAATGGCGGTACAGAGGTTGCCAACCGCGAGGGGAGCTAATCTCAGAA 1254
 Db 1198 ACCTAATACAAATGGCGGTACAGAGGTTGCCAACCGCGAGGGGAGCTAATCTCAGAA 1257
 QY 1255 AGCGCTGCTAGTCCGGATCGGAGTCTGCAATCGACTCCGTGAAGTCGGAATCGCTAGT 1314
 Db 1258 AGCACTGCTAGTCCGGATCGGAGTCTGCAATCGACTCCGTGAAGTCGGAATCGCTAGT 1317
 QY 1315 AATCGCGATACAGATGTCGCGGTGAATACGTTCCCGGGTCTTGTATACACCGCCCGTCA 1374
 Db 1318 AATCGCGATACAGATGTCGCGGTGAATACGTTCCCGGGTCTTGTATACACCGCCCGTCA 1377
 QY 1375 CACCATGGAGTGGGTTTACAGAGACGAGTGTCTTAACCGTAAAGGAGGCGCTTGCCA 1434
 Db 1378 CACCATGGAGTGGGTTTACAGAGACGAGTGTCTTAACCGTAAAGGAGGCGCTTGCCA 1437
 QY 1435 CGGTGAGATTCACTAGCTGGGGTG 1457
 Db 1438 CGGTGAGATTCACTAGCTGGGGTG 1460

RESULT 11
 ADM32707
 .ID ADM32707 standard; DNA; 1460 BP.

XX ADM32707;
 AC 17-JUN-2004 (first entry)
 XX AOB_Type C R5clone47 16S rDNA.
 XX 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
 KW aqueous environment; freshwater; seawater; aquarium; ss.
 XX Nitrosomonas sp.
 XX WO2004026772-A2.
 XX 01-APR-2004.
 XX 10-SEP-2003; 2003WO-US028210.
 XX 19-SEP-2002; 2002US-0386217P.
 PR 19-SEP-2002; 2002US-0386218P.
 PR 19-SEP-2002; 2002US-0386219P.
 XX (AQUA-) AQUARIA INC.
 XX Hovanec TA;
 XX WPI, 2004-304936/28.
 XX New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 of ammonia in aqueous environment.
 XX Disclosure; Page 12; 98pp; English.
 XX This sequence represents a 16S rDNA sequence derived from an ammonia
 CC oxidising bacteria (AOB). This sequence may be used in a composition
 CC which comprises an isolated bacterial strain that oxidizes ammonia to
 CC nitrite. The composition may be used for alleviating or preventing the
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least
 CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.
 XX Sequence 1460 BP; 388 A; 316 C; 454 G; 302 T; 0 U; 0 Other;
 SQ
 Query Match 84.4%; Score 1230.2; DB 12; Length 1460;
 Best Local Similarity 92.3%; Pred. No. 0;
 Matches 1351; Conservative. 0; Mismatches 103; Indels 9; Gaps 5;
 QY 1 ATTGAACTGCGCGCATGCTTTACATGCAATGCAAGTCGAACGCGACACGATGCTTCAT 60
 Db 1 ATTGAACTGCGCGCATGCTTTACATGCAATGCAAGTCGAACGCGACG--CGGGGCTTCGCG 58
 QY 61 CTGTGGCGAGTGGCGGACGGGTGAGTAAATGATCGAATCGAATCGAAGAGGGGGTA 120
 Db 59 CTGCGCGAGTGGCGGACGGGTGAGTAAATGATCGAATCGAATCGAAGAGGGGGTA 118
 QY 121 ACGCATGAAAGATGTGCTAATACCGCATATATCTTAAGAGGAAAGACAGGGGATCGAAA 180
 Db 119 ACGCATGAAAGATGTGCTAATACCGCATAT-CTCTGAGGAGAAAGACAGGGGATCGCAA 177
 QY 181 GACCTTGGCTTTGGAGCGCGGATGCTGATAGCTAGTGTGGTGGGTAAGGCGCTAC 240
 Db 178 GACCTTGGCTTTAAAGGAGCGCGGATGCTGATAGCTAGTGTGGTGGGTAAGGCGCTAC 237
 QY 241 CAAGCGGACGATCAGTGTGCTGAGAGGACGACCGACCATCTGGGACTGAGACAG 300
 Db 238 CAAGCGGACGATCAGTGTGCTGAGAGGACGACCGACCATCTGGGACTGAGACAG 297
 QY 301 GCCCAGACTCTTACGGGAGGACGAGTGGGGAATTTTGGACAATGGGCGCAAGCTGATC 360
 Db 298 GCCCAGACTCTTACGGGAGGACGAGTGGGGAATTTTGGACAATGGGCGCAAGCTGATC 357

QY 121 ACGCATCGAAGATGTGCTAATACCGCATATCTTAAAGCGAAGACGAGGATCGAA 180
 Db |||||
 QY 128 ACGTACGAAAGATTACGCTAATACCGCATATCTTAAAGCGAAGACGAGGATCGAA 187
 Db |||||
 QY 181 GACCTTGGCTTTTGGAGCGCGGATGTCTGATTAGCTAGTTGGTGGGTAAGAGCCCTAC 240
 Db |||||
 QY 188 GACCTCTCGCTTTCGAGCGCGGATGTCTGATTAGCTAGTTGGTGGGTAAGAGCCCTAC 247
 Db |||||
 QY 241 CAAAGCGGACGATCAGTATGTTGTTGAGAGGACGACGACGACGACGACGACGACG 300
 Db |||||
 QY 248 CAAAGCGGACGATCAGTATGTTGAGAGGACGACGACGACGACGACGACGACGACG 307
 Db |||||
 QY 301 GCCAGACTCTTACGCGGACGACGAGTGGGATTTTGGACAAATGGCGGACGCTGATC 360
 Db |||||
 QY 308 GCCAGACTCTTACGCGGACGACGAGTGGGATTTTGGACAAATGGCGGACGCTGATC 367
 Db |||||
 QY 361 CAGCAATGCCGCTGAGTGAAGAGCCCTTCGGGTTGTAAGCTCTTTCAGTCTGAGAAGA 420
 Db |||||
 QY 368 CAGCCATGCCGCTGAGTGAAGAGCCCTTCGGGTTGTAAGCTCTTTCAGTCTGAGAAGA 427
 Db |||||
 QY 421 AAGGTTAGGTAATATCGTATCATGAGGATCGATGAGGATCGATGAGGATCGATGAGG 480
 Db |||||
 QY 428 AATGCGCGCTCTAATACATAGCGTGTGATGAGGATCGATGAGGATCGATGAGGATCG 487
 Db |||||
 QY 481 TACGTGCGCAGCGCGGCTTATAGTGTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCG 540
 Db |||||
 QY 488 TACGTGCGCAGCGCGGCTTATAGTGTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCG 547
 Db |||||
 QY 541 AAGGCTGCGCAGCGCGGCTTATAGTGTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCG 600
 Db |||||
 QY 548 AAGGCTGCGCAGCGCGGCTTATAGTGTAGGTCGAGGTCGAGGTCGAGGTCGAGGTCG 607
 Db |||||
 QY 601 TGGCTTTGAACTA CAAGCTTAGAGTGTGCGAGAGGAGGAGGAGGAGGAGGAGGAGG 660
 Db |||||
 QY 608 GGCCTTTGAGACTGACGCGCTAGAGTGTGACAGAGGAGGAGGAGGAGGAGGAGGAGG 667
 Db |||||
 QY 661 TGAATGCTGAGATATGGAAGATATGAGTGTGAGGTCGAGGTCGAGGTCGAGGTCGAG 720
 Db |||||
 QY 668 TGAATGCTGAGATATGGAAGATATGAGTGTGAGGTCGAGGTCGAGGTCGAGGTCGAG 727
 Db |||||
 QY 721 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGATACCTGCTGATGTCACGCC 780
 Db |||||
 QY 728 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGATACCTGCTGATGTCACGCC 787
 Db |||||
 QY 781 CTAAGCATGTCACTAGTGTGTTGG - GCCTTATTAGGCTTGTAAACGAGTAAACGGGT 838
 Db |||||
 QY 788 CTAAGCATGTCACTAGTGTGTTGGGAGGTTAAACCTCTTAGTGTCTAGTAAACGGGT 847
 Db |||||
 QY 839 GAAAGTTGACCGCTGCGGAGTACGCTGCAAGATTAAACCTCAAGGAAATGACGGGAC 898
 Db |||||
 QY 848 GAAAGTTGACCGCTGCGGAGTACGCTGCAAGATTAAACCTCAAGGAAATGACGGGAC 907
 Db |||||
 QY 899 CCGCAACAGCGTGGATTATGTGATTAATTCGATGCAACGCGAAGAAACCTTACCTACCC 958
 Db |||||
 QY 908 CCGCAACAGCGTGGATTATGTGATTAATTCGATGCAACGCGAAGAAACCTTACCTACCC 967
 Db |||||
 QY 959 TTGACATGTAGGAAATTTCTAGAGATAGATTAGTGC - - - TTGCGGAACGCTAACACAGG 1015
 Db |||||
 QY 968 TTGACATGTAGGAAATTTCTAGAGATAGATTAGTGC - - - TTGCGGAACGCTAACACAGG 1027
 Db |||||
 QY 1016 TGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
 Db |||||
 QY 1028 TGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
 Db |||||
 QY 1076 CAACCTTGTTCATTAATTTGCTATCATTTTGGTGGGCACTTTAATGAGACTGCGGCTGACA 1135
 Db |||||
 QY 1088 CAACCTTGTTCATTAATTTGCTATCATTTTGGTGGGCACTTTAATGAGACTGCGGCTGACA 1147
 Db |||||
 QY 1136 AACCGGAGAAAGTGGGATGACGCTCAAGTCTCTATGCGCCCTTATGGGTAGGCTTACACA 1195
 Db |||||
 QY 1148 AACCGGAGAAAGTGGGATGACGCTCAAGTCTCTATGCGCCCTTATGGGTAGGCTTACACA 1207
 Db |||||
 QY 1196 CGTAATACATGCGCGTACAGAGGTTGCCAACCCGCGAGGGAGGTAATCTCAGAA 1255
 Db |||||

Db 1208 CGTCATACATGCTCGGTTTACAGGGTTGCCAACCCGCGAGGGAGCCATCTCAGAAA 1267
 QY 1256 GCGGCTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTTGAAGTCGGAATCGTAGTA 1315
 Db 1268 GCGGATCGTAGTCCGGATTCGAGTCTGCAACTCGACTGTCATGGAAGTCGGAATCGTAGTA 1327
 QY 1316 ATCCGGATCAGCATGTCGGGTGAATACGTTCCGGGTCTTGTACACACGCGCGTCAC 1375
 Db 1328 ATCCGGATCAGCATGTCGGGTGAATACGTTCCGGGTCTTGTACACACGCGCGTCAC 1387
 QY 1376 ACCATGCGAGTGGGTTTCCACAGAACGAGGTAGTCTAACCCGTAAGGAGGCGCTTGCCAC 1435
 Db 1388 ACCATGCGAGGCGGTTCTGCCAAGAAGTAGTAGCTTAACCCGTAAGGAGGCGCTTGCCAC 1447
 QY 1436 GGTGAGATTATGACTCGGGTG 1457
 Db 1448 GCGCGGTTCTGACTGGGGTG 1469

RESULT 13
 ABQ78660
 ID ABQ78660 standard; DNA; 1495 BP.
 XX AC ABQ78660;
 XX AC
 DT 25-NOV-2002 (first entry)
 XX Nucleotide sequence of a fragment of 16S rDNA gene.
 DE 16S rDNA; nitrogen oxide; nitrogen; ss.
 KW Denitromonas aromaticus.
 OS Denitromonas aromaticus.
 XX JP2002142755-A.
 XX 21-MAY-2002.
 XX 14-NOV-2000; 2000JP-00346844.
 XX 14-NOV-2000; 2000JP-00346844.
 XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
 PA (BIOI-) BIOINDUSTRY KYOKAI SH.
 PA (AJIN) AJINOMOTO KK.
 XX WPI; 2002-611517/66.
 XX Microorganism belonging to Denitromonas for removal of nitrogen oxide by reduction of nitrogen oxide to nitrogen in gas or aqueous solution, has specific mycological characters.
 PT Disclosure; Page 6-7; 8pp; Japanese.
 XX The present sequence represents a fragment of 16S rDNA gene of Denitromonas aromaticus. This is a novel microorganism belonging to the new genus Denitromonas, and which has specific mycological characters. The new microorganism efficiently reduces and removes nitrogen oxide. The bacterium is used for the removal of nitrogen oxide. It reduces nitrogen oxide to nitrogen in a gas or aqueous solution
 XX Sequence 1495 BP; 363 A; 350 C; 483 G; 299 T; 0 U; 0 Other;
 SQ

Query Match 82.2%; Score 1197.2; DB 6; Length 1495;
 Best Local Similarity 89.7%; Pred. No. 0;
 Matches 1309; Conservative 0; Mismatches 148; Indels 3; Gaps 2;
 QY 1 ATTGAACGCTGGCGCATGCTTTACATCATGCACTCAAGTCGAACGCGACGAGGATGCTTGCAT 60
 Db 16 ATTGAACGCTGGCGCATGCTTTACATCATGCACTCAAGTCGAACGCGACGAGGATGCTTGC 75
 QY 61 CTGTGCGGAGTGGCGGACGCGGTGAGTAATGCAATCGGAAGCTATCCAGAGAGGGGGTA 120
 Db |||||

Db 76 CTGGTGGCGAGTGGCGAAGCGGGTGAATGTCATCGGAACGTACCCAGTAGTGGGGGATA 135
 Qy 121 ACCGATCGAAAGATGTCTTAATACCGCATATATCTTAAGAGAGAAAGACGGGGATCGAAA 180
 Db 136 GCGCGGCGAAAGCGGATTAATACCGCATATATCTTAAGAGAGAAAGACGGGGACCTTCG 195
 Qy 181 GACCTTGGCCCTTTGGAGCGCGGATGTCTGATTAGCTAGTTGGTGGGTAAAGGCGCTAC 240
 Db 196 GCGCTCGCCCTACTGGAGCGGCTGATGTGCGATTAGCTAGTTGGTGGGTAAAGGCGCTAC 255
 Qy 241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCGACCATCTGGGACTGAGACAG 300
 Db 256 CAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACAG 315
 Qy 301 GCCCAGACTCTACGGGAGGACGACGTGGGGAATTTTGGACAAATGGGCCCAAGCCTGATC 360
 Db 316 GCCCAGACTCTACGGGAGGACGACGTGGGGAATTTTGGACAAATGGGCCCAAGCCTGATC 375
 Qy 361 CAGCAATGCGCGTGAGTCAAGAGGCGCTTCGGTTGTAAAGCTCTTTCAGTTCGAGAGA 420
 Db 376 CAGCCATGCGCGTGAGTGAAGAGGCGCTTCGGTTGTAAAGCTCTTTCAGTTCGAGAGA 435
 Qy 421 AAAGGTTACGGTAAATAATCGTGACTCATGACGTATCGACAGAGGAGTATCGACAGAGAACCGCGCTAAC 480
 Db 436 AATCATGCGCCCCGATACCGGCGGTGATGACGGTACCATCAGAGAGAACACCGGCTAAC 495
 Qy 481 TAGTGGCCAGACGCGCGGTATATCGTAGGGTGCAAGCGTTAATTCGGAATTAATCTGGGCGT 540
 Db 496 TAGTGGCCAGACGCGCGGTATATCGTAGGGTGCGAGCGTTAATTCGGAATTAATCTGGGCGT 555
 Qy 541 AAAGGTTGCGCAGGCGGCTTTGTAGTCAGATGTGAATCCCGGCGCTTAACCTCGGAAT 600
 Db 556 AAAGGTTGCGCAGGCGGCTTTGTAGTCAGATGTGAATCCCGGCGCTTAACCTCGGAAT 615
 Qy 601 TCGCTTTGAAATACAAAGCTAGAGTGTGCGAGAGGAGGTGGAATTCATGTGTAGCAG 660
 Db 616 TCGCTTTGACTGACGCGTAGAGTACGCGAGAGGCGGTGGAATTCACGTGTAGCAG 675
 Qy 661 TGAATGCTAGAGATATGGAAGAACATCGATGGCGAAGCGAGCTCTCTGGGTTAACTACT 720
 Db 676 TGAATGCTAGAGATATGGAAGAACACCGATGGCGAAGCGAGCTCTCTGGGCTGTACT 735
 Qy 721 GACGCTCATGCAAGAGCGTGGGAGGACAAACAGGATAGATACCTGTGTAGTCCACGCC 780
 Db 736 GACGCTCATGCAAGAGCGTGGGAGGACAAACAGGATAGATACCTGTGTAGTCCACGCC 795
 Qy 781 TTAACGAGTGTCAACTAGTTGTT--GGGCTTTATTAGGCTTGGTAAACGAAGCTAACCGGT 838
 Db 796 CTAAACGATGTCACTAGTTGTTTCGGAGAGGAACTTTCTGGGTAAACGAGCTAACCGGT 855
 Qy 839 GAAGTTGACCGCTCGGGAGTACGCTGCGAAGATTAAAACTCAAAAGGAATTGACCGGGAC 898
 Db 856 GAAGTTGACCGCTCGGGAGTACGCTGCGAAGATTAAAACTCAAAAGGAATTGACCGGGAC 915
 Qy 899 CGCACAAGCGGTGATATGTGGATTAAATTCGATGCAACGCGAAGAAACCTTACCTACCC 958
 Db 916 CGCACAAGCGGTGATATGTGGATTAAATTCGATGCAACGCGAAGAAACCTTACCTACCC 975
 Qy 959 TTGACATGTAGCGAATTTTCTAGAGATAGATTAGTG-CTTCGGGAACGCTTAACACAGGTG 1017
 Db 976 TTGACATGTCTGGAATTTGTGAGAGATCACTTGGTGCCTTCGGGAGCGAGAACACAGGTG 1035
 Qy 1018 CTGATGCGTGTGCTAGCTCGTGTGAGATGTGGGTTAAGTCCCGCAACGAGCGCA 1077
 Db 1036 CTGATGCGTGTGCTAGCTCGTGTGAGATGTGGGTTAAGTCCCGCAACGAGCGCA 1095
 Qy 1078 ACCCTTGTCAATTAATGTCATTTGTTGGGCACTTTAATGACATGCGCGGTACACAA 1137
 Db 1096 ACCCTTGTCAATTAATGTCATTTGTTGGGCACTTTAATGACATGCGCGGTACACAA 1155
 Qy 1138 CCGAGGAGGTTGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTCACACG 1197
 Db 1156 CCGAGGAGGTTGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTCACACG 1215

Qy 1198 TAATACAATGGCGGTACAGAGGGTTGCCAACCCCGAGGGGAGTAAATCTCAGAAAGC 1257
 Db 1216 TCATACAATGGTTCGATACAGAGGGTTGCCAACCCCGAGGGTCCCAATCCAGAAAGC 1275
 Qy 1258 GCGTGTAGTCCGATCGGAGTCTCAACTCGACTCCGTGAAGTCGGAATCGTACTAAT 1317
 Db 1276 CGATCGTGTAGTCCGATTCGAGTCTCAACTCGACTCCATGAAGTCGGAATCGTACTAAT 1335
 Qy 1318 CCGGATCAGCATGTTCGCGGTGAATACGTTCGCGGTCTTGTACACACCGCCCGTCCACAC 1377
 Db 1336 CCGGATCAGCATGTTCGCGGTGAATACGTTCGCGGTCTTGTACACACCGCCCGTCCACAC 1395
 Qy 1378 CATGGAGTGGTTTACACAGAGCAGGTAGTCTTAACCGTAAGAGGGCGCTTGCACCG 1437
 Db 1396 CATGGAGTGGTTTACACAGAGTAGTGTAACTTCGGGAGGGCGCTTACACCG 1455
 Qy 1438 TGAGATTTCATGACTGGGGTG 1457
 Db 1456 TGAGATTTCATGACTGGGGTG 1475

RESULT 14

AAC86026

ID AAC86026 standard; cDNA; 1460 BP.

XX AAC86026;

XX AC AAC86026;

XX 06-AUG-2003 (revised)

DT 29-AUG-2001 (first entry)

XX 16S rDNA, SBRA220.

XX 16S rDNA; polyphosphate accumulating organism; PAO; probe; primer;

XX detection; phosphorus; waste water; sludge; ss.

XX Unidentified.

XX W0200146459-A1.

XX 28-JUN-2001.

XX 28-DEC-2000; 2000WO-AU001611.

XX 23-DEC-1999; 99AU-00004867.

XX (CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.

XX Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;

XX WPI; 2001-408656/43.

XX Novel oligonucleotide probe or primer useful for detecting polyphosphate

XX accumulating organism in a sample, comprises a sequence that is unique to

XX 16S rDNA of polyphosphate accumulating organisms.

XX Claim 4; Fig 3; 54pp; English.

XX The sequences given in AAC86021-30 represent 16S rDNA sequences from

XX polyphosphate accumulating organisms (PAOs). Sequences which are unique

XX to these 16S rDNA sequences are used to create a probe or primer for

XX detecting the relevant organisms. The primer/probe sequences are useful

XX for detecting PAO cells in a sample, by treating cells with the primer/probe

XX to fix cellular contents, contacting fixed cells with the primer/probe which

XX is labelled with a radiolabel, a reporter group or a hapten, under the

XX conditions which allow the probe to hybridize with 16S rRNA within the

XX fixed cell, removing unhybridized probe from the fixed cells, and

XX detecting the labeled probe-RNA hybrid by fluorescence in situ

XX hybridization. The primer/probe sequences are useful for identifying PAOs

XX that are capable of biologically removing phosphorus from waste water.

XX Rapid assessment of the presence of a number of PAOs in a waste water

XX sample, can be done using the primer/probe sequences. They allow quick

XX and convenient assessment of whether a sludge or waste water sample

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Result No.	Score	Query	Length	DB	ID	Description
1	1149.2	78.9	1522	11	US-11-198-242-2	Sequence 2, Appli
2	1142.8	78.4	1526	11	US-11-198-242-1	Sequence 1, Appli
3	1089.6	74.8	1405	9	US-10-515-311-5	Sequence 5, Appli
4	1021.8	70.1	1501	9	US-10-513-639-1	Sequence 1, Appli
5	1031.2	70.1	1493	9	US-10-831-2864-4668	Sequence 4868, A
6	1030.2	70.0	1508	9	US-10-831-2864-4665	Sequence 4865, A
7	1019.8	70.0	1510	9	US-10-831-2864-4660	Sequence 4860, A
8	1019.6	70.0	1494	9	US-10-831-2864-4661	Sequence 4861, A
9	1018	69.9	1507	9	US-10-831-2864-4667	Sequence 4867, A
10	1017	69.9	1508	9	US-10-831-2864-4664	Sequence 4864, A
11	1015.4	69.7	1510	9	US-10-831-2864-4662	Sequence 4862, A
12	1008.4	69.2	1530	9	US-10-831-2864-4667	Sequence 4867, A
13	1007.2	69.1	1492	9	US-10-831-2864-4668	Sequence 4868, A
14	1007.2	69.1	1531	9	US-10-831-2864-4667	Sequence 4867, A
15	1005.4	69.0	1495	9	US-10-831-2864-4665	Sequence 4865, A
16	1005.2	69.0	1494	9	US-10-831-2864-4665	Sequence 4865, A
17	1005.2	69.0	1503	9	US-10-831-2864-4666	Sequence 4866, A
18	1005.2	69.0	1514	9	US-10-831-2864-4666	Sequence 4866, A

19	1004.8	69.0	1494.	9	US-10-831-2866A-48676	A	Sequence 48676, A
20	1003.8	68.9	1535.3	9	US-10-831-2866A-48670	A	Sequence 48670, A
21	1003.6	68.9	1501	9	US-10-831-2866A-48670	A	Sequence 48670, A
22	1002.8	68.8	1527	9	US-10-831-2866A-48653	A	Sequence 48653, A
23	1000	68.6	1486	9	US-10-831-2866A-48679	A	Sequence 48679, A
24	995.2	68.3	1542	11	US-09-941-035-158	App	Sequence 158, App
25	995.2	68.3	1542	11	US-11-198-794-158	App	Sequence 158, App
26	995.2	68.3	1542	11	US-11-198-794-158	App	Sequence 158, App
27	993.2	68.3	1542	11	US-11-198-657-158	App	Sequence 158, App
28	990	67.9	1533	9	US-10-831-2866A-48668	A	Sequence 48668, A
29	988	67.8	1418	9	US-10-831-2866A-48651	A	Sequence 48651, A
30	988	67.8	1418	9	US-10-831-2866A-48652	A	Sequence 48652, A
31	981.2	67.3	1436	9	US-10-831-2866A-48667	A	Sequence 48667, A
32	979.8	67.2	1481	9	US-10-831-2866A-48672	A	Sequence 48672, A
33	977.8	67.1	1525	9	US-10-831-2866A-48689	A	Sequence 48689, A
34	850.4	58.4	1485	14	US-11-055-637-76	App	Sequence 76, App
35	848.4	58.3	1513	14	US-11-055-637-79	App	Sequence 79, App
36	845.8	58.1	1505	14	US-11-055-637-80	App	Sequence 80, App
37	841.2	57.7	1509	11	US-11-273-617-6	App	Sequence 6, App
38	839.6	57.6	1486	14	US-11-055-637-69	App	Sequence 69, App
39	838.6	57.6	1545	14	US-11-055-637-66	App	Sequence 66, App
40	837.2	57.5	1587	11	US-11-273-617-8	App	Sequence 8, App
41	837.2	57.5	1486	14	US-11-055-637-71	App	Sequence 71, App
42	837.2	57.5	1507	14	US-11-055-637-78	App	Sequence 78, App
43	837	57.4	3169	8	US-10-793-626-3356	App	Sequence 3356, App
44	837	57.4	3308	8	US-10-793-626-3905	App	Sequence 3905, App
45	837	57.4	3657	8	US-10-793-626-4187	App	Sequence 4187, App

ALIGNMENTS

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RESULT 1
US-11-198-242-2
; Sequence 2, Application US/11/98242
; Publication No. US20060035345A1
;
GENERAL INFORMATION:
; APPLICANT: AJINOMOTO CO., INC.
; TITLE OF INVENTION: Processes for the production of beta-amino acids by using acylase
; FILE REFERENCE: AB04037
; CURRENT APPLICATION NUMBER: US/11/198,242
; CURRENT FILING DATE: 2005-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
;
; LENGTH: 1522
;
; TYPE: DNA
;
; ORGANISM: Burkholderia sp.
; FEATURE:
; NAME/KEY: 16S rDNA
; LOCATION: (1)..(1522)
;
; OTHER INFORMATION:
;
US-11-198-242-2

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Query Match	78.9%;	Score 1149.2;	DB 11;	Length 1522;
Best Local Similarity	88.2%;	Pred. No. 0;		
Matches 1287;	Conservative	0;	Mismatches 163;	Indels 10;
				Gaps 3;

Oy 1 TTGTAACGCTGGCGGCATGCTTTACACATGCAAGTCGAAACGGCAGACGGAGTCTGCAT 60
 Db 20 ATTGAACCTGACGGCATGCCCTTACACATGCAAGTCGAAACGGCAGCGCGGCAAC-- 77
 Oy 61 CTGGTGGCGAATGGCGGACGGGTGAGTATGCATGCGAACGTATCCAGAAAGAGGGGGGTA 120
 Db 78 CTGGCGGGGAAATGGCGGAACGGGTGAGTAAATCATGGAACGTCTCTGTAAAGTGGGGGAT 137
 Oy 121 ACGCATGGAANGATGTGCTAATACCGCATATATCTTAAAGAGGAAAGCAGGGGATCGAAA 180
 Db 138 GCCCGCGCAAAAGCCGAGTAAATACCGCATACGCTCTACAGGAAAGGGGGGAGATTGAG 197
 Oy 181 GACCTTGGGCTTTTGGAGCGGCCCATATGCTAATTAAGTAGTGTGAGGGGTAAAGGCTTAC 240
 Db 198 GACCTTCTGCTACAGGGCGGCCCATATGCTAATTAAGTGTGAGGGGTAAAGGCTTAC 257

Oy	241	CAAAGCCACGATCACTAGTGTGGTCTGAGAAAGACAACAAGCCACACTGGGACTGAGACACG	300
Db	258	CAAGGCGACGATCTGTACTGCTGTGAAAGAGACGACAGCCACACTGGGACTGAGACACG	317
Oy	301	GCCGACACTCTTACGGGAGGACGACGAGTGGGGAAATTTTGACAAATGGGCGCAAGCTGTATC	360
Db	318	GCCGACACTCTTACGGGAGGACGACGAGTGGGGAAATTTTGACAAATGGGCGCAAGCTGTATC	377
Oy	361	CAGCAATGCCCGGTGAGTGAAGAAAGGCTTTGGGTTGTAAGCTCTTCAATCGAGAA	420
Db	378	CAGCAATGCCCGGTGTGTGAAGAAAGGCTTTGGGTTGTAAGCACTTTTGTCCGAAAGA	437
Oy	421	AAAGGTTACGGTTAATAATTCGTGACTCTGACCGGATTCAGACAGAAAGACACCGGCTAAC	480
Db	438	AAAGCGCGGTGTTAATACCCTGTGGCGAGTACCGGTAACCGAAAGAAATAGCACCGGCTAAC	497
Oy	481	TACGTGCAGACGCCCGCGTAATACGTAGGGTGCACGCTTAATCGGAATTACTGGCGGT	540
Db	498	TACGTGCAGACGCCCGCGTAATACGTAGGGTGCACAGGCTTAATCGGAATTACTGGCGGT	557
Oy	541	AAAGGGTGCAGAGCGCGCTTTGTAAGTACAGATGTGAATTCGCCGGGCTTAACTCGGGAAT	600
Db	558	AAAGCGTGCAGAGCGCGCTTCGCTAAGACAGATGTGAATTCGCCGGGCTTAACTCGGGAAC	617
Oy	601	TGCGTTTGAAACTACAAAGCTAGAGTGTGCAGAGAGAGTGGAAATTCATGTGTACAG	660
Db	618	TGCAATTTGTGACTGGCGGGCTAGAGTATGGCAGAGGGGGTGTAAATTCAGTGTAGCAG	677
Oy	661	TGAAATGGGTGAGATATGGAAGAACATTCGATGGGAAAGGACGCTCTTGGGTTAAACAT	720
Db	678	TGAAATGGGTGAGATATGGAAGAAATACGATGGGAAAGGACGCCCCCTGGGCCCAATCT	737
Oy	721	GACGCTATGACAGAAACGTTGGGAGACAAACAGGATTAGATACCCTGTAGTCCACGCC	780
Db	738	GACGCTATGACAGAAACGTTGGGAGACAAACAGGATTAGATACCCTGTAGTCCACGCC	797
Oy	781	CTAAACGATGTCACTAGTTGTTGGGCTTATTAGGCTTTGGTAACGAAGCTTACGCGTGA	840
Db	798	CTAAACGATGTCACTAGTTGTTGGGAGTTCAATTCCTTAAGTAAGTGTAGCTAACGCCGTGA	857
Oy	841	AGTTGACCGGCTGGGGAGTAACGCTGTGCAAGATTTAAATCTCAAGGAATTGACGGGACCC	900
Db	858	AGTTGACCGGCTGGGGAGTAACGCTGTGCAAGATTTAAATCTCAAGGAATTGACGGGACCC	917
Oy	901	GCACAAGCGGTGATTATGTGATTAATTCGATGCAACGCCGCAAAAACCTTACCTTACCCTT	960
Db	918	GCACAAGCGGTGATTATGTGATTAATTCGATGCAACGCCGCAAAAACCTTACCTTACCCTT	977
Oy	961	GACATGTAGCGAATTTTCTAAGAGATAGATTAGTGC---TTGGGGAACGCTAACACAGGTG	1017
Db	978	GACATGTATGAAATCTCTCTAGAGAGTGGGAGTCCCGAAGGGAGCCATTAACACAGGTG	1037
Oy	1018	CTGCATGCGCTGTCTCAGCTCGTGTGCGTAGATGTTGGGTTTAAGTCCCGCACAGACGCA	1077
Db	1038	CTGCATGCGCTGTCTCAGCTCGTGTGCGTAGATGTTGGGTTTAAGTCCCGCACAGACGCA	1097
Oy	1078	ACCCTGTTCATTAATTGCAATCATTTGGTGGGCACTTTAATGAGACTGCGCGGTACAA	1137
Db	1098	ACCCTGTTCCTTAACTAGTTGCTTAC----GCAGAAGCACTCTAGGGAGACATCGCGGTACAA	1152
Oy	1138	CCGAGGAAGAGTGGGAGTAGAGTCAAGTCTCATATGGCCCTTAATGGGTAGGGCTTACACG	1197
Db	1153	CCGAGGAAGAGTGGGAGTAGAGTCAAGTCTCATATGGCCCTTAATGGGTAGGGCTTACACG	1212
Oy	1198	TAAATCAATGGCGCGCTACAGAGGATTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGC	1257
Db	1213	TCATATCAATGGCGCGAACAAGAGGTCGCGCAACCCGCGAGGGGAGCCATCCACAGAAAC	1272
Oy	1258	GCGTGTATGTCCGGATTCGGAATCTGCAACTGCACTCCGATGAAGTGGGAATGCGTATGAT	1317
Db	1273	GCGTGTATGTCCGGATTCGCACTCTGTCAATCTGCAATGCGGAATGCGGAATGCGTATGAT	1333

Qy	1318	CGGGGATCAGCAGCTCGCGGTGAAATACGTTCCCGGGCTTGTAACAACCGCGCTCACAC	1377
Db	1333	CGCGGATCACACATCCCGCGGTGATACGTTCCCGGGCTTGTAACAACCGCGCTCACAC	1392
Qy	1378	CATGGGATGGGGTTTCAACGAAGCAGGTAGTCTAACCGTAAGAGAGGAGCGCTTGCCACGG	1437
Db	1393	CATGGGATGGGGTTTACCAAGAACTGGCTAGTCTAACCGCAAGGAGGACGGTACCAACGG	1452
Qy	1438	TGAGATTCACTACTGGGGTG	1457
Db	1453	TAGGATTCACTACTGGGGTG	1472

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RESULT 2
US-11-198-242-1
; Sequence 1, Application US/11198242
; Publication No. US20060035345A1
; GENERAL INFORMATION:
; APPLICANT: AJINOMOTO CO., INC.
; TITLE OF INVENTION: Process for the production of beta-amino acids by using acylase
; FILE REFERENCE: ABO4037
; CURRENT APPLICATION NUMBER: US/11/198,242
; CURRENT FILING DATE: 2005-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1526
; TYPE: DNA
; ORGANISM: Variovorax sp.
; FEATURE:
; NAME/KEY: 16S rDNA
; LOCATION: (1)..(1526)
; OTHER INFORMATION:
US-11-198-242-1

```

Query Match	Similarity	78.4%	Score 1142.8	DB 11	Length 1526
Best Local	87.8%	Pred. No. 0			
Matches 1282	Conservative	0	Mismatches 172	Indels 6	Gaps 3
QY	1	ATTGACGCTGGCCGACATGCTTTACACATGCAAGTCGAA	CGCGACGACGACGATGCTTGAT	60	
Db	20	ATTGACGCTGGCCGACATGCTTTACACATGCAAGTCGAA	CGCGACGACGCGCGGAGCAATC--	77	
QY	61	CTGCTGGCACTGGCCGACCGGCTGATGAATATGCAATCG	AATCTCAGAAAGGGGGGTA	120	
Db	78	CTGCGCGGAGATGGCCGAA	CGGGTGATGAATAACATCGGAACGTGCCAATCGTGGGGGATA	137	
QY	121	ACGCATCGAAGAATGTGCTAATACCGGATATATCTTAAG	AGAGAAACAGGGGATCGAAA	180	
Db	138	ACGCAGCGAAGCTGTGCTAATACCGATACGATCTACGA	TGAAGAACAGGGGATCCGCA	197	
QY	181	GACCTTGCGCTTTTGGAGCGCGCGATGCTTGATTAGCT	TAAGTTGGTGGGATGAAGGCTTAC	240	
Db	198	GACCTTGCGCGAATGAGAGCGCGCGATGAGCATTAAG	CTAGTTGGTGAAGTGAAGGCTTAC	257	
QY	241	CAAGGCGACGATCGATGATGTGTGTGAGAGAGACGAC	CAAGCGACACTGAGACACG	300	
Db	258	CAAGCTTTCGATCTGTAGCTGTGTGAGAGAGACGAC	CAAGCGACACTGAGACTGAGACAGC	317	
QY	301	GCCGAGACTCTTACGGGAGGCGACGACGTGGGAAATTT	TGACAAATGGGCGCAAGCCTGATC	360	
Db	318	GCCGAGACTCTTACGGGAGGCGACGACGTGGGAAATTT	TGACAAATGGGCGCAAGCCTGATC	377	
QY	361	CAGCAATGCCGCGTGAATGAAGAAGGCTTCGGGTTGTA	AAAGCTCTTCAATCGAAGAA	420	
Db	378	CAGCCATGCCCGCGTGAATGAAGAAGGCTTCGGGTTGTA	AAGCTCTTGTATCGAAGAA	437	
QY	421	AAAGGTAACGGTAATATATCGTGAATCATACGATATCG	ACAGAAAGACACCGGCTAAC	480	
Db	438	AAAGGCTCTTCTAATAAAGAGGGCTAATGACGTTAC	CGTAAGAAATAAGCACCGGCTAAC	497	
QY	481	TACGTGCCAGACGCCCGGCTAATCGTAGGCTGAACGTT	AATCGGAATTAACCTGGGCT	540	

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Db 498 TAGGTGACGAGAGCGGGGTAATAGTAGGGTGAAGCGTTAATCGGAATTACTGGGGT 557
Qy 541 AAAGGTCGCGAGCGGCTTTGTAAGTCAGATGTGAAATCCCGGGCTTAACTGGGAAT 600
Db 558 AAAGCGCGCCAGCGGCTGATGTAAGACAGTTGTGAAATCCCGGGCTCAACTGGGAAC 617
Qy 601 TGGCTTTGAACCTACAGAGGCTAGAGTGTGGCAGAGGGAGGTAATTCATGTGTAGAG 660
Db 618 TGCATCTGTGACCTGACCTGAGTAGAGGAGGAGGGGAGTGAATTCGGGTGTAGAG 677
Qy 661 TGAATGCGTAGAGATATGAAAGAACATCATGAGCGGAGAGCGCTCGGGTTAACT 720
Db 678 TGAATGCGTAGAGATATGAAAGAACATCATGAGCGGAGAGCGGAGAGCGGAGAG 737
Qy 721 GAGGCTCATGACGAAAGCGTGGGAGAGAAACAGATTAATACCTGTGTAGTCCAGCC 780
Db 738 GAGGCTCATGACGAAAGCGTGGGAGAGAAACAGATTAATACCTGTGTAGTCCAGCC 797
Qy 781 CTAAAGCATGTCACTGATGTTGGGCTTATTAGGCTGTGTAAGAGCTTAAGCGCGTGA 840
Db 798 CTAAAGCATGTCACTGATGTTGGGCTTATTAGGCTGTGTAAGAGCTTAAGCGCGTGA 857
Qy 841 AGTTGACCGGCTGGGAGTAGAGTCCGACAGATTAAATCTCAAGAAATTTGACGGGAGCC 900
Db 858 AGTTGACCGGCTGGGAGTAGAGTCCGACAGATTAAATCTCAAGAAATTTGACGGGAGCC 917
Qy 901 GCAAGACGGTGGATTATGTGAAATTAATTCAGTCAACGCGAAACCTTAACCTT 960
Db 918 GCAAGACGGTGGATTATGTGAAATTAATTCAGTCAACGCGAAACCTTAACCTT 977
Qy 961 GACATGAGGGAATTTCTAGAGATAGATTAGTCT---TGGGAGAGCTTAACAGCAGGTG 1017
Db 978 GACATGAGGGAATTTCTAGAGATAGATTAGTCT---TGGGAGAGCTTAACAGCAGGTG 1037
Qy 1018 CTGCATGCTGTGCTCAGCTGATGCTGAGATGTTGGGTTAATCCCGCAACGAGGCA 1077
Db 1038 CTGCATGCTGTGCTCAGCTGATGCTGAGATGTTGGGTTAATCCCGCAACGAGGCA 1097
Qy 1078 ACCCTGTCAATTAATGCTCATTTGGTGGGCACTTTAATGAGCTGCGGTGACAA 1137
Db 1098 ACCCTGTCAATTAATGCTCATTTGGTGGGCACTTTAATGAGCTGCGGTGACAA 1156
Qy 1138 CCGGAGAGAGTGGGAGTAGAGTCAATCCCTCATGCGCTTATGGTGAAGGGCTTCAACG 1197
Db 1157 CCGGAGAGAGTGGGAGTAGAGTCAATCCCTCATGCGCTTATGGTGAAGGGCTTCAACG 1216
Qy 1198 TAATACATGAGCGGTACAGAGGTTGCCAACCCGCGAGGGAGAGTAACTCAGAAAGC 1257
Db 1217 TCATACATGAGCGGTACAGAGGTTGCCAACCCGCGAGGGAGAGTAACTCAGAAAGC 1276
Qy 1258 GCGTGTGATGCTCGAGTCCGAGTCCGAACTGCACTCGGTGAAGTGGAAATCGCTAAT 1317
Db 1277 CAGTGTGATGCTCGAGTCCGAGTCCGAACTGCACTCGGTGAAGTGGAAATCGCTAAT 1336
Qy 1318 CCGGAGTACAGATGCGCGGTGAATACGTTCCCGGGCTTTGTAACAACCGCCGTCAAC 1377
Db 1337 CCGGAGTACAGATGCGCGGTGAATACGTTCCCGGGCTTTGTAACAACCGCCGTCAAC 1396
Qy 1378 CATGAGAGTGGGTTTCAACAGAGCAGGTAGTAACTGTAAGAGAGGGCGCTTGGCAGG 1437
Db 1397 CATGAGAGTGGGTTTCAACAGAGCAGGTAGTAACTGTAAGAGAGGGCGCTTGGCAGG 1456
Qy 1438 TGAGATTATGACTGGGGT 1457
Db 1457 CAGGTTCTGTAGCTGGGGT 1476

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RESULT 3
 US-10-515-311-5
 ; Sequence 5, Application US/10515311
 ; Publication No. US20060030021A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Turner, Susan J

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; TITLE OF INVENTION: Novel Microorganisms and Uses Therefor
; FILE REFERENCE: 11752-006US1
; CURRENT APPLICATION NUMBER: US/10/515,311
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: PCT/NZ2003/000100
; PRIOR FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: NZ 519137
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Acidivoxax temperans
; US-10-515-311-5

Query Match      74.8%; Score 1089.6; DB 9; Length 1405;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1233; Conservative 0; Mismatches 169; Indels 12; Gaps 3;

Qy 18 TGCCTTAACATGCAAGTCAAGCGACGAGATGCTGATCTGTGGCGAGTGGCGG 77
Db 1 TGCCTTAACATGCAAGTCAAGCGATAC---AGGCTTGGATGCTGACGAGTGGCGA 56
Qy 78 ACGGGTAGATTAATGATCGGAGCGTATCCAGAAAGAGGGGGTAAACGATCGAAAGATGTG 137
Db 57 ACGGGTAGATTAATGATCGGAGCGTATCCAGATGCTGGGGATTAACGAGCGAAAGCTTTG 116
Qy 138 CTAAATCCGATTAATCTTAAGAGAGAAACAGAGGATCGAAAGACTTGGCTTTTGA 197
Db 117 CTAAATCCGATTAATCTTAAGAGAGAAACAGAGGATCGAAAGACTTGGCTTTTGA 176
Qy 198 GCGGCGGATGCTGATTAAGTGTGTTGGGTTAAAGGCTTACCAAGCGAGATCACTA 257
Db 177 GCGGCGGATGCTGATTAAGTGTGTTGGGTTAAAGGCTTACCAAGCGAGATCACTA 236
Qy 258 GTTGTGCTGAGAGAGAGCAAGCCACACTGGGAGCTGAGACAGGCGCAAGCTCTACGGG 317
Db 237 GTTGTGCTGAGAGAGAGCAAGCCACACTGGGAGCTGAGAGCTGAGAGCTCTACGGG 296
Qy 318 AGGACAGTGGGGAATTTTGGCAATGGGCGCAAGCTGATCAGCAATGCCCGGTGAG 377
Db 297 AGGACAGTGGGGAATTTTGGCAATGGGCGAAACCTGATCAGCAATGCCCGGTGCA 356
Qy 378 TGAAGAGGCTTGGGTTGTAAGCTCTTTCACTGAGAGAGAAAGTTACGCTAATA 437
Db 357 GATGAGAGGCTTGGGTTGTAAGCTCTTTGTAAGAGAGAAAGTCTGCTTAATA 416
Qy 438 ATGTGACTGATGAGGATTCGACAGAGAGAGCGGCTTAATGAGTGCAGAGCGG 497
Db 417 CTTGGGATCAGTACGATCCGTAAGAAATGACAGCGGCTTAATGAGTGCAGAGCGG 476
Qy 498 GGTAAATACGATGAGGTCAGAGCTTAATCGAAATTAATGAGGCTTAAGAGGTCGAGCGG 557
Db 477 GGTAAATACGATGAGGTCAGAGCTTAATCGAAATTAATGAGGCTTAAGAGGTCGAGCGG 536
Qy 558 CTTTGAAGTCAATGTAATTCGCGGCTTAACCTGAGAAATTTGGCTTTGAACCTA 617
Db 537 TTAATAAAGACATGTAATTCGCGGCTTAACCTGAGAAATTTGGCTTTGATGCTAT 596
Qy 618 GGTAAAGTGTGAGAGAGAGGAGTGAATTCATGATGTGAGCTGAATTCGAGAGATA 677
Db 597 AGCTAAGTGTGAGAGAGAGGAGTGAATTCGCGGTGTGAGCTGAATTCGAGAGATA 656
Qy 678 TGAAGAACATGATGCGAGAGAGCTCTCTGGGTTAACTGAGCTCATGACAGAA 737
Db 657 CCGAGGAACACGATGCGAGAGAGCAATCCCTGGGCTGTATGAGCTCATGACAGAA 716
Qy 738 GCGTGGGAGCAACAGATTAGATACCTGTGTAGTCCAGCGCTTAAGATGTAACATG 797
Db 717 GCGTGGGAGCAACAGATTAGATACCTGTGTAGTCCAGCGCTTAAGATGTAACATG 776
Qy 798 GTTGTGGGCTTAATGAGCTTGTGTAAGAGACTTAAGCGGTGAAGTTGACCGGCTGGGA 857

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Db      777 GTTGTGGGCTCTCACTGACCTAGTAAGAGCTTAAGCGGTAAGTGAACGCGCTGGGGA 836
Qy      858 GTACGGCTCGAAGATTAATACTCAAGAGAAATTGAACGGGGAACCCGCAAGCGGTGATTA 917
Db      837 GTACGGCCGCAAGGTTGAACTCAAGAGAAATTGAACGGGGAACCCGCAAGCGGTGATTA 896
Qy      918 TGTGATTAATTGCAACGCGAAGAAACCTTAACCTTGAATGATGATGATGATGATGAT 977
Db      897 TGTGATTAATTGCAACGCGAAGAAACCTTAACCTTGAATGATGATGATGATGATGAT 956
Qy      978 CTGAGATTAATTGATCT---TCGGAAACGCTTAACAGGTGATGATGATGATGATGAT 1034
Db      957 TTGAGAGTAAGAGAGTCTGAAAGAGAGCGTAACAGGTGATGATGATGATGATGAT 1016
Qy      1035 GCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1094
Db      1017 GCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076
Qy      1095 CCATCATTTGGTGGGCACTTTAATGAGACTGCGGTGACAAACCGAGAGAGGTGGGGA 1154
Db      1077 C-----TACGAAAGGGCACTTAATGAGACTGCGGTGACAAACCGAGAGAGGTGGGGA 1131
Qy      1155 TGAAGTAACTCCCTATGAGGCTTATGAGGCTTCAACGATTAATCAATGAGCGGTA 1214
Db      1132 TGAAGTAACTCCCTATGAGGCTTATGAGGCTTCAACGATTAATCAATGAGCGGTA 1191
Qy      1215 CAGAGGTTGCAACCCGCGAGGGAGCTAATCTCAGAAAGCGGCTGATGATGATGATGATGAT 1274
Db      1192 CAGAGGTTGCAACCCGCGAGGGAGCTAATCTCAGAAAGCGGCTGATGATGATGATGATGAT 1251
Qy      1275 GAGGTTGCAACTGATCTCGGTGAAGTGGATGCTAATGCTGATGATGATGATGATGATGAT 1334
Db      1252 GAGGTTGCAACTGATCTCGGTGAAGTGGATGCTAATGCTGATGATGATGATGATGATGAT 1311
Qy      1335 CGGTAATAGGTTCCCGGGCTTTGTACACACCGCGCTCAACCATGGAGTGGGTTTCA 1394
Db      1312 CGGTAATAGGTTCCCGGGCTTTGTACACACCGCGCTCAACCATGGAGTGGGTTTCTG 1371
Qy      1395 CCAGAGCAGATAGTCTTAACCGTAAGAGAGGCGC 1428
Db      1372 CCAGAGCAGATAGTCTTAACCGTAAGAGAGGCGC 1405

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RESULT 4
US-10-513-639-1

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; Sequence 1, Application US/10513639
; Publication No. US20060010511A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yicheng
; APPLICANT: Chen, Yancheng
; APPLICANT: Li, Fengmei
; APPLICANT: Tian, Zhexian
; APPLICANT: Lin, Min
; APPLICANT: Wang, Xiping
; TITLE OF INVENTION: NOVEL GLYPHOSATE-TOLERANT
; TITLE OF INVENTION: 5-ENOPIRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE AND THE GENE
; FILE REFERENCE: 18495-002US1
; CURRENT APPLICATION NUMBER: US/10/513, 639
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: CN 02117991.3
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: CN 02117647.7
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: PCT/CN02/00539
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas putida P.P4G-1

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US-10-513-639-1
Query Match      70.1%; Score 1021.8; DB 9; Length 1501;
Best Local Similarity 83.0%; Pred. No. 1,6e-309;
Matches 1213; Conservative 0; Mismatches 242; Indels 6; Gaps 4;

Qy      1 ATTGAACGCGGCGGATGCTTTACATGATGAGTGAACGCGAGCAGCATCTTGCAT 60.
Db      21 ATTGAACGCGTGGCGGAGGCTTAACATGATGAGTGAACGCGAGCAGCATCTTGCAT 80
Qy      61 CTGTGGCGAGTGGCGGAGGCTTAATGATGAGTGAACGCGAGCAGCATCTTGCAT 120
Db      81 TCATTT--CAGCGCGGAGGCGGAGTGAATGCTGAGTGAATGCTGAGTGGGAGCA 138
Qy      121 AGCATGCAAGATGTGCTTAATCCCATTAATCTTAAGAGAGAAACGCGGAGTGA 180
Db      139 AGCTTTCGAAGAGAGATTAATCCCATTAATGCTTACCGGAGAGAAACGCGGAGTGA 198
Qy      181 GACCTTGCGCTTTTGAAGGGGCGGATGCTGATTAATGCTGATGATGATGATGATGATGAT 240
Db      199 GGCCTTGCGCTTAATGATGAGCTTGAATGATGATGATGATGATGATGATGATGATGAT 258
Qy      241 CAGGCGAGATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db      259 CAGGCGAGATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 318
Qy      301 GCCCAATCTCTTACGGGAGGAGCAGATGAGGAGATTTTGAACATGAGGCGCAACCTGATC 360
Db      319 GTCCAGATCTCTTACGGGAGGAGCAGATGAGGAGATTTTGAACATGAGGCGCAACCTGATC 378
Qy      361 CAGCAATGCGGCGTGAAGTGAAGAGGCTTGGGTTTGAAGGCTTTTCAAGTGAAGAGA 420
Db      379 CAGCAATGCGGCGTGAAGTGAAGAGGCTTGGGTTTGAAGGCTTTTCAAGTGAAGAGA 438
Qy      421 AAGGTTAAGGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db      439 AAGGTTAAGGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 498
Qy      481 TACGTGCGAGCAGCGCGGCTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db      499 TCTGTGCGAGCAGCGCGGCTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 558
Qy      541 AAGGTTGCGGAGGCGGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db      559 AAGGTTGCGGAGGCGGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 618
Qy      601 TCGGTTTGAACCTTAACAGGCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db      619 TGTATCAAAACTGGAAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
Qy      661 TGAATGCGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db      679 TGAATGCGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 728
Qy      721 GAGGCTCAGGAGCAAGAGGTTGGGAGCAACAGATTAATGATGATGATGATGATGATGATGAT 780
Db      739 GAGGCTCAGGAGGAGAGGTTGGGAGCAACAGATTAATGATGATGATGATGATGATGATGAT 788
Qy      781 CTAAAGATGCTAACTAGTGTGTTGGGCTTATTAAG--GCTTGTGAAGAGCTTAACCGGTG 839
Db      799 GTAAAGATGCTAACTAGTGTGTTGGGCTTATTAAG--GCTTGTGAAGAGCTTAACCGGTG 858
Qy      840 AAGTTACCGGCTGGGAGTACGCTGCGAAGTTAAATCTCAAGAGAAATTGACGGGAGC 899
Db      859 AAGTTACCGGCTGGGAGTACGCTGCGAAGTTAAATCTCAAGAGAAATTGACGGGAGC 918
Qy      900 CGCAGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
Db      919 CGCAGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 978
Qy      960 TGAATGAGAGAAATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1018
Db      979 TGAATGAGAGAAATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038

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QY 1019 TGCATGCTGTCCTGACGTCGTGTCGAGAGATGTTGGTTAAGTCCCGCAACGAGCGCA 1078
 DB 1039 TGCATGCTGTCCTGACGTCGTGTCGAGAGATGTTGGTTAAGTCCCGCAACGAGCGCA 1098
 QY 1079 CCTTTCATTAATTTGCGCATCA--TTTGGTTGGGCACTTTAATGAGACTGCGGTCACAA 1136
 DB 1099 CCTTTCATTAATTTGCGCATCA--TTTGGTTGGGCACTTTAATGAGACTGCGGTCACAA 1158
 QY 1137 ACCGAGAGAGAGTGGGAGATGACGTCAAGTCTCATGCGCTTTAATGGGATGGCTTCAAC 1196
 DB 1159 ACCGAGAGAGAGTGGGAGATGACGTCAAGTCTCATGCGCTTTAATGGGATGGCTTCAAC 1218
 QY 1197 GTATACAAATGGGCGGTACAGAGAGGTTGCGAACCGCGAGGGGAGGCTAATCTGAGAA 1256
 DB 1219 GTGCTACAAATGGGCGGTACAGAGAGGTTGCGAACCGCGAGGGGAGGCTAATCTGAGAA 1278
 QY 1257 CGCGTCGTAGTCCCGATCGAGTGCACACTGCACTCCGTGAGAGTCCGATCGCTAGTAA 1316
 DB 1279 CGCATCTGATGTCGGATCGAGTGCACACTGCACTCCGTGAGAGTCCGATCGCTAGTAA 1338
 QY 1317 TCGCGATCAGCATGTCGCGGTGAATACGTTCCCGGTCTTGTACACACCGCCGTCA 1376
 DB 1339 TCGCGATCAGCATGTCGCGGTGAATACGTTCCCGGTCTTGTACACACCGCCGTCA 1398
 QY 1377 CCATGGAGAGCGGTTTCAACGAGAGCGTGTCTAACCCGTAAGAGGCGCTTGCCACG 1436
 DB 1399 CCATGGAGAGCGGTTTCAACGAGAGCGTGTCTAACCCGTAAGAGGCGCTTGCCACG 1458
 QY 1437 GTGAGATTCACTGCTGGGGTG 1457
 DB 1459 GTGAGATTCACTGCTGGGGTG 1479

RESULT 5

US-10-831-286A-48683
 ; Sequence 48683, Application US/10831286A
 ; Publication No. US20060046246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZENG, QIANDONG
 ; APPLICANT: CHATELIER, SONIA
 ; APPLICANT: MOIR, DONALD T.
 ; APPLICANT: LACROIX, BRUNA
 ; APPLICANT: CHIDRESS, DARRELL
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
 ; FILE REFERENCE: 032796-174.001
 ; CURRENT APPLICATION NUMBER: US/10/831.286A
 ; PRIOR FILING DATE: 2004-04-26
 ; PRIOR APPLICATION NUMBER: 60/464,955
 ; NUMBER OF SEQ ID NOS: 48788
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 48683
 ; LENGTH: 1493
 ; TYPE: DNA
 ; ORGANISM: *Parlousa dispersa*
 US-10-831-286A-48683

Query Match 70.1%; Score 1021.2; DB 9; Length 1493;
 Best Local Similarity 82.9%; Pred. No. 2.5e-309;
 Matches 1214; Conservative 0; Mismatches 243; Indels 7; Gaps 4;

QY 1 ATGGAACGCTGGCGGATGCTTTACATGCAATGCAAGTCAACGCGACGAGTCTTG--- 57
 DB 1 ATGGAACGCTGGCGGCGGCTTACATGCAATGCAACGCGACGAGAGGCTTTC 60
 QY 58 -CATCTGGGCGAGTGGCGGAGCGGAGTGAATGCAATCGGAAGCTATCCGAGAGAGG 116
 DB 61 TCTTTGGGTGGCGAGTGGCGGAGCGGAGTGAATGCTTGGGAACTCCCGATGGAAGG 120
 QY 117 GGTAAACCATCGAAAGATGTGTCTAATACCGCATATCTTAAAGAGAGAAAGCAGGGATC 176
 DB 121 GATTAATCTAGTGAAGAGTGTGTCTAATACCGCATATCTTAAAGAGAGAAAGTGGGAGCC 180

QY 177 GAAAGACCTTGGCGCTTTTGGAGCGCGCATGCTGATTTAGCTAGTTGGTGGGTAAGGC 236
 DB 181 TTTGGGCTTCAACCATCGGATGTGTCCAGATGGATTTAGTGGGTAATGCG 240
 QY 237 CTACCAAGCGAGATCAGTATGTTGGTCTGAGAGAGCAACCAAGCACTCTGGA 296
 DB 241 TCACTTAGGAGATCTCTAGCTGGTCTGAGAGATGACCAAGCACTCTGGA 300
 QY 297 CAGGCGCCAGACTCTTACGGGAGGAGCAGTGGGGAATTTTGAACAATGGGCGCAAGCT 356
 DB 301 CAGGCTCCAGACTCTTACGGGAGGAGCAGTGGGGAATTTTGAACAATGGGCGCAAGCT 360
 QY 357 GATCCAGCAATGCGCGGTGAGTGAAGAGGCTTCCGGTTGTAAGCTTTTCAAGTCGAG 416
 DB 361 GATCCAGCAATGCGCGGTGATGAAGAGGCTTCCGGTTGTAAGCTTTTCAAGTCGAG 420
 QY 417 AAGAAAGGTTACGATTAATATCTGACTCATGACGATTCGACAGAGAGCAACCGGC 476
 DB 421 AAGAAAGGTTACGATTAATATCTGACTCATGACGATTCGACAGAGAGCAACCGGC 480
 QY 477 TAACTAGTCCAGCAGCGCGGTAAATGCTAGGGTGCAGAGCTTAATGGAAATTA 536
 DB 481 TAACTAGTCCAGCAGCGCGGTAAATGCTAGGGTGCAGAGCTTAATGGAAATTA 540
 QY 537 GCGTAAAGGTTGGGCGAGCGCGCTTTGTAAGTCAAGTGTGAATCCCGGCTTAACTGG 596
 DB 541 GCGTAAAGGTTGGGCGAGCGCGCTTTGTAAGTCAAGTGTGAATCCCGGCTTAACTGG 600
 QY 597 GAATTCGTTTGAATCAACAGGCTAGAGTGTGGCAGAGGAGGTGAATTCATGTGTA 656
 DB 601 GAATTCGTTTGAATCAACAGGCTAGAGTGTGGCAGAGGAGGTGAATTCATGTGTA 660
 QY 657 GCAATGAAATGCTAGATATGAAAGACATGATGGCGAAGGCAAGCTTCTGGGTTAA 716
 DB 661 GCGGTAAATGCTAGATATGAAAGACATGATGGCGAAGGCAAGCTTCTGGGTTAA 720
 QY 717 CACTGACGCTCAGACAGAAAGGTTGGGAGCAACAGATTAGTAACTCTGGTGAATGCA 776
 DB 721 GACTGACGCTCAGAGTGAAGAGGTTGGGAGCAACAGATTAGTAACTCTGGTGAATGCA 780
 QY 777 CGCCTTAAACGATGCACTAGTGTGGGCTTATTAAGCTTGG-TAAAGAACTAAGC 835
 DB 781 CGCCTTAAACGATGCACTAGTGTGGGCTTATTAAGCTTGG-TAAAGAACTAAGC 840
 QY 836 CGTGAAGTTGACCGCTGGGAGTACGCTGCGAAGTTAACTCAAGAAATTTGACGG 895
 DB 841 CGTGAAGTTGACCGCTGGGAGTACGCTGCGAAGTTAACTCAAGAAATTTGACGG 900
 QY 896 GACCCGCAAGCGGTGAGATTATGTTGATTAATGATGCAAGCGAAACCTTACCTA 955
 DB 901 GACCCGCAAGCGGTGAGATTATGTTGATTAATGATGCAAGCGAAACCTTACCTA 960
 QY 956 CCTTACATATGACGAATTTTCTAGAGATGATTAAGTCTTCCGGAACGCTTACAG 1014
 DB 961 GCTTACATATGACGAATTTTCTAGAGATGATTAAGTCTTCCGGAACGCTTACAG 1020
 QY 1015 GTGCTGATGCTGTGCTGCACTGCTGTGCTGAGATGTTGGTTAAGTCCGCAACGAGC 1074
 DB 1021 GTGCTGATGCTGTGCTGCACTGCTGTGCTGAGATGTTGGTTAAGTCCGCAACGAGC 1080
 QY 1075 GCAACCTTGTCACTTAATGTCATC-AATTGGTGGGCACTTAAAGAGACTGCGGTGA 1133
 DB 1081 GCAACCTTGTCTTGTGTCAGAGCGGTTCGCGGAACTCAAGAGACTGCGGTGA 1140
 QY 1134 CAACCGGAGAGAGTGGGAGATGACGTCAAGTCTTATGAGTGGTGAAGGCTTCA 1193
 DB 1141 TAAACGGAGAGAGTGGGAGATGACGTCAAGTCTTATGAGTGGTGAAGGCTTCA 1200
 QY 1194 CAGCTAATACATGAGCGGTACAGAGGTTTCCCAACCGCGAGGAGGAGCTAATCTCAGA 1253
 DB 1201 CAGCTAATACATGAGCGGTACAGAGGTTTCCCAACCGCGAGGAGGAGCTAATCTCAGA 1260

SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 48681
 LENGTH: 1494
 TYPE: DNA
 ORGANISM: Pantoea dispersa
 US-10-831-286A-48681

Query Match 70.0%; Score 1019.6; DB 9; Length 1494;
 Best Local Similarity 82.9%; Pred. No. 8e-309;
 Matches 1213; Conservative 0; Mismatches 244; Indels 7; Gaps 4;

1 ATGAAGCGCTGGCGGAGTGTGTTAATGATGCAAGTGGAGCGAGCGATGTTG--- 57
 1 ATGAAGCGCTGGCGGAGTGTGTTAATGATGCAAGTGGAGCGAGCGATGTTGCG 60
 58 -CATCTGGTGGCGAGTGGCGGAGCGGATGATGATGATGATGATGATGATGATG 116
 61 TCTTTGGTGGCGAGTGGCGGAGCGGATGATGATGATGATGATGATGATGATG 120
 117 GGTAAAGCATGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 176
 121 GATTAAGCATGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 180
 177 GAAAGCATGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 236
 181 TGGGCGCTGCAACCATGATGATGATGATGATGATGATGATGATGATGATG 240
 237 CTACCAAGCGAGCATGATGATGATGATGATGATGATGATGATGATGATG 296
 241 TCACTAAGCGAGCATGATGATGATGATGATGATGATGATGATGATGATG 300
 297 CAGCGCCAGATCTCTAAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 356
 301 CAGCGCTCAAGCTCTAAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 360
 357 GATCAAGCATGCGCGGATGATGATGATGATGATGATGATGATGATGATG 416
 361 GATCAAGCATGCGCGGATGATGATGATGATGATGATGATGATGATGATG 420
 417 AAGAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 476
 421 AAGAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 480
 477 TAACTAAGCGAGCATGATGATGATGATGATGATGATGATGATGATGATG 536
 481 TAACTAAGCGAGCATGATGATGATGATGATGATGATGATGATGATGATG 540
 537 GCGTAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 596
 541 GCGTAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 600
 597 GAAATGCGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 656
 601 GAAATGCGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 660
 657 GCAAGTAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTA 716
 661 GCGTAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 720
 717 CACTGAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 776
 721 GACTGAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 780
 777 GCGCTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 835
 781 GCGCTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 840
 836 CGTGAAGTAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTT 895
 841 CGTGAAGTAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTT 900
 896 GACCCGACAAAGCGGATGATGATGATGATGATGATGATGATGATGATGATG 955

901 GCGCCGACAAAGCGGATGATGATGATGATGATGATGATGATGATGATG 960
 956 CCTTGAAGTAAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1014
 961 GCGCTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1020
 1015 GTCGTCAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1074
 1021 GTCGTCAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1080
 1075 GCAAGCTTGAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1133
 1081 GCAAGCTTGAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1140
 1134 CAAAGCGAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1193
 1141 TAAAGCGAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1200
 1194 CAGTAAATCAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1253
 1201 CAGTAAATCAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGGTTAAGG 1260
 1254 AAGCGGCTGAAGTCCGATGCGAGTCTGCAACTGCACTCGTGAAGTGGATG 1313
 1261 AAGTGGCTGAAGTCCGATGCGAGTCTGCAACTGCACTCGTGAAGTGGATG 1320
 1314 TAAAGCGAGTCAAGTGGTGGTGAATGATGATGATGATGATGATGATGATG 1373
 1321 TAAAGCGAGTCAAGTGGTGGTGAATGATGATGATGATGATGATGATGATG 1380
 1374 ACAAGTGGAGGTTTACACAGAGAGGATGCTAAGCTGAAGGAGGCGTTGCC 1433
 1381 ACAAGTGGAGGTTTACACAGAGAGGATGCTAAGCTGAAGGAGGCGTTGCC 1440
 1434 ACGGTGAGATTGATGATGATGATGATGATGATGATGATGATGATGATG 1457
 1441 ACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1464

RESULT 9
 US-10-831-286A-48677
 ; Sequence 48677, Application US/10831286A
 ; Publication No. US20060046246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZENG, QIANDONG
 ; APPLICANT: CHATELLIER, SONIA
 ; APPLICANT: MOIR, DONALD T.
 ; APPLICANT: LACROIX, BRUNA
 ; APPLICANT: CHILDRESS, DARRELL
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
 ; FILE REFERENCE: 032796-174.001
 ; CURRENT APPLICATION NUMBER: US/10/831, 286A
 ; PRIOR FILING DATE: 2004-04-26
 ; PRIOR APPLICATION NUMBER: 60/464,955
 ; NUMBER OF SEQ ID NOS: 48788
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 48677
 ; LENGTH: 1507
 ; TYPE: DNA
 ; ORGANISM: Providencia rettgeri
 US-10-831-286A-48677

Query Match 69.9%; Score 1018; DB 9; Length 1507;
 Best Local Similarity 83.2%; Pred. No. 2.6e-308;
 Matches 1217; Conservative 0; Mismatches 240; Indels 5; Gaps 5;

1 ATGAAGCGCTGGCGGAGTGTGTTAATGATGCAAGTGGAGCGAGCGATGTTG 59
 11 ATGAAGCGCTGGCGGAGTGTGTTAATGATGCAAGTGGAGCGAGCGATGTTG 70
 60 TCTGG-TGGCGAGTGGCGGAGTGTGATGATGATGATGATGATGATGATGATG 118

Db 71 TCTGCTGACGAGCGCGGACCGGTGATGTAATGTATGAGGATCTCCGCAATGAGGGGGA 130
Qy 119 TTAAGCATCGAAAGATGTGCTAATACCGCATTAATCTTAAGGAGAAAGCAGGGGATGGA 178
Db 131 TTAACCATCGGAAACGGTGGCTAATACCGCATTAATCTTAAGGAGAAAGCAGGGGAACTT 190
Qy 179 AAGACCTTGCGCTTTTGGAGCGGCGATGTCATTAAGTATGTTGGTGGGTAAGGCGCT 238
Db 191 CGGTCTTGCGCTATCGAATGAACCCATATAGGGAATTAAGTATGTTGGTGGGTAAGGCGCTC 250
Qy 239 ACCAAGGCGACGATCAGTATGTTGGTCTGAGAGGACGACGACACTGGGACTGAGACA 298
Db 251 ACCTAGGCGACGATCCTAGCTGGTCTGAGAGGATGATCAGGCACTGGGACTGAGACA 310
Qy 299 CGGCGCAGACTCTTAACGGGAGGACGATGGGGAAATTTTGGACATGGGCGGCAAGCTTGA 358
Db 311 CGGCGCAGACTCTTAACGGGAGGACGATGGGGAAATTAATGCAATGGGCGGCAAGCTTGA 370
Qy 359 TCCAGCAATGCGCGGTGATGAAAGAGGCTTCGGGTTGTAAGGCTTTTCAGTCAAGAA 418
Db 371 TGCAGCCATGCGCGGTGATGAAAGAGGCTTCGGGTTGTAAGGCTTTTCAGTCAAGAA 430
Qy 419 GAAAGGTTACGTAATATCTGATCATGACGGTATCGACAGAGAGCACCGGCTA 478
Db 431 GAAAGGTTATGCTAATATCATCAACGATTGACGTTACCGACAGAGAGCACCGGCTA 490
Qy 479 ACTACGTCCGACGACCGCGGTAAATAGTAGGGTCCAGGCTTAATCGGAATTAATCTGGGC 538
Db 491 ACTCGGTCCGACGACCGCGGTAAATAGTAGGGTCCAGGCTTAATCGGAATTAATCTGGGC 550
Qy 539 GTAAAGGTTGCGGACGCGGCTTTGTAAGTCAAGTGTAAATCCCGGCGCTTAACCTGAGGA 598
Db 551 GTAAAGGTTGCGGACGCGGCTTTGTAAGTCAAGTGTAAATCCCGGCGCTTAACCTGAGGA 610
Qy 599 ATTCGCTTGAATCTAACGCTAGATGTGACAGAGGAGGTGGAAATTCATGTGTAGC 658
Db 611 ATTCGCTTGAATCTAACGCTAGATGTGACAGAGGAGGTGGAAATTCATGTGTAGC 670
Qy 659 AGTAAATGCTTAAGATATGGAAGAAATGATGTGCGAAGGACGCTTCCTGGTTAAACA 718
Db 671 GGTAAATGCTTAAGATATGGAAGAAATGATGTGCGAAGGACGCTTCCTGGTTAAACA 730
Qy 719 CTGACGCTCATGCAAGAAAGGCGGAGCAAAACAGATTAGATTCCTGGTATGCGACG 778
Db 731 CTGACGCTCATGCGAAGGCGGAGCAAAACAGATTAGATTCCTGGTATGCGACG 790
Qy 779 CCTTAAACGATGTC-AACTAGTGTGGGCTTATTAAGCTTGTGTAACGAAGCTTAACGCG 837
Db 791 CTGTAACGATGTGATTTGAGGTTGTTCCCTAGAGAGTGGCTTCGGAAGCTTAACGCG 850
Qy 838 TGAAGTTGACCGCTCGGGAAGTACGCTGCAAGTTAAATCTCAAGGAATTTGACGGGGA 897
Db 851 TTAATATGACCGCTCGGGAAGTACGCGCAAGGTTAAATCTCAATGAATTTGACGGGGA 910
Qy 898 CCGGCAAGAGCGGTGATTAATGGAATTAATTCGATGCAAGCGGAAACCTTAACCTACC 957
Db 911 CCGGCAAGAGCGGTGATGATGTGTTAATTCGATGCAAGCGGAAACCTTAACCTACC 970
Qy 958 CTGACATGTAGCGAATTTTCTAGAGATGAATTAATG-CTTCGGGAAGCTTAACAGAGT 1016
Db 971 CTGACATGTAGCGAATTTTCTAGAGATGAATTAATG-CTTCGGGAAGCTTAACAGAGT 1030
Qy 1017 GCTGCAATGCTGTGTGATGCTGTGTGTGTAAGTGTGGTTAAGTCCCGCAAGAGCGC 1076
Db 1031 GCTGCAATGCTGTGTGATGCTGTGTGTGTAAGTGTGGTTAAGTCCCGCAAGAGCGC 1090
Qy 1077 AACCTTGTCAATTAATGCAATC-ATTGTTGGGCACTTAATAGAGCTCCGCTGACA 1135
Db 1091 AACCTTGTCTTGTGTCAGGCAATACGTCGGGAATCAAGAGAGCTCCGCTGATA 1150
Qy 1136 AACCGAGAGAGGTGGGATGACGTCAATGCGCTTAATGGTGAAGGCTTCA 1195
Db 1151 AACCGAGAGAGGTGGGATGACGTCAATGCGCTTAATGGTGAAGGCTTCA 1210

Qy 1196 CGTAAATCAATGCGCGGTACAGAGGTTGGCCACCCGAGAGGGGAGTAACTCAGAAA 1255
Db 1211 CGTCTCAATGCGGTATACAAAGAGCACTCCGAGAGCAAGCGGAATCATATAA 1270
Qy 1256 GCGGCTGTAGTCCGATTCGAGTCTGCAACTCGACTCCGTGAAGTCGGAATGCTAGTA 1315
Db 1271 GTACTGTAGTCCGATTCGAGTCTGCAACTCGACTCGAATGAGTCCGGAATGCTAGTA 1330
Qy 1316 ATCGCGATCAGCATGTCCGCGTAATACGTTCCCGGCTTTGATACACACCGCGCTGAC 1375
Db 1331 ATCGTATCAGAAATGCTACGTAATACGTTCCCGGCTTTGATACACACCGCGCTGAC 1390
Qy 1376 ACCATGGAGTGGGTTTCAAGAGAGGATGCTAACCGTAAAGAGGCGCTTGGCAC 1435
Db 1391 ACCATGGAGTGGGTTTCAAGAGAGGATGCTAACCGTAAAGAGGCGCTTGGCAC 1450
Qy 1436 GGTGAGATTCATGACTGGGTTG 1457
Db 1451 TTTGTATTCATGACTGGGTTG 1472

RESULT 10
US-10-831-286A-48684
Sequence 48684, Application US/10831286A
Publication No. US20060046246A1
GENERAL INFORMATION:
APPLICANT: ZENG, QIANDONG
APPLICANT: CHATELIER, SONIA
APPLICANT: MOIR, DONALD T.
APPLICANT: LACROIX, BRUNA
APPLICANT: CHILDRESS, DARRELL
TITLE OR INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
FILE REFERENCE: 032796-174.001
CURRENT APPLICATION NUMBER: US/10/831,286A
CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: 60/464,955
PRIOR FILING DATE: 2003-04-24
NUMBER OF SEQ ID NOS: 48788
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48684
LENGTH: 1508
TYPE: DNA
ORGANISM: *Providencia rustigianii*
US-10-831-286A-48684

Query Match 69.8%; Score 1017; DB 9; Length 1508;
Best Local Similarity 83.2%; Pred. No. 5.3e-308;
Matches 1217; Conservative 0; Mismatches 240; Indels 6; Gaps 5;

Qy 1 ATGGAACGCTGGCGGCACTGCTTACACATGCAAGTGCAGCGACAC-GGATGCTTGCA 59
Db 11 ATGGAACGCTGGCGGCGGCACTGCTTACACATGCAAGTGCAGCGGAAAGCTTGCT 70
Qy 60 TCGG-TCGGAGAGGCGGCGGCGGAGTGAATGATCGAAGCATCAGAAAGAGGGGG 118
Db 71 TCTGCTGACGAGCGGCGGCGGCGGAGTGAATGATGATGAGGAACTTCCCGCATAGAGGGGGA 130
Qy 119 TAAAGCATCGAAAGATGTGCTTAATACCGCATTAATCTTAAGAGAGAAAGCAGGGGATCGA 178
Db 131 TAACTACTGAAACGGTAGTAAATACCGCATTAATCTTTGAGAGCAAGAGGGGAATT 190
Qy 179 AAGACCTTGGGCTTTTGGAGCGGCGCATGCTGATTAAGTAAAGTGTGGGTAAAGGCTT 238
Db 191 CGGTCTTGGGCTTAATGAGGAACCAATATGGAATTAAGTGTGGGTAAAGGCTT 250
Qy 239 ACCAAGCGCGATCAGTATGTTGTTGAGAGGACGACGACACTGGGACTGAGACA 298
Db 251 ACCAAGCGCGATCAGTATGTTGTTGAGAGGACGACGACACTGGGACTGAGACA 310
Qy 299 CGGCGCAGACTCTTAACGGGAGGACGAGATGGGAAATTTTGAACAATGGGCGCAAGCTTGA 358
Db 311 CGGCGCAGACTCTTAACGGGAGGACGAGATGGGAAATTTTGAACAATGGGCGCAAGCTTGA 370


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Oy 597 GAATTCGTTGAACCTAACAAGCTAGTGTGAGAGGAGGAGTGAATTCATGTGA 656
Db 611 GAATGGCATCTTAACTGGTCAGCTAGACTCTTGTAGAGGGAGGTAGATTCATGTGA 670
Oy 657 GCAAGTAAATGCGTAGATATGAGAAACATCATGATGCGAAGGAGCCTCTGGGTAA 716
Db 671 GCGGTGAATGCGTAGATGAGAAATACCGGTGGGAGAGCGGCCCTGAGCAAA 730
Oy 717 CACTGACGCTCATGACGAAACCGTGGGAGCAACAGATTTAGTACCTTGGTGTCCA 776
Db 731 GACTGACGCTCATGAGCGAAGACCGTGGGAGCAACAGATTTAGTACCTTGGTGTCCA 790
Oy 777 CGCCCTAAACAGATGCACTAGTGTGGGCTTTATAGGCTTGG-TAAGAAAGCTAAAG 835
Db 791 CGCTGTAAACAGATGCACTAGTGTGGGCTTTATAGGCTTGGCTTCCGAGCTTAAAG 850
Oy 836 CGTGAAGTTGACCGGCTGGGAGTACCGTTCGCAAGATTAAACCTCAAGAAATTGACGG 895
Db 851 CGTTAAATCGACCGCTGGGAGTACCGGCTGCAAGATTAAACCTCAAGAAATTGACGG 910
Oy 896 GACCGGCAAGCGGTGATATGTGATTAATTGATGCAACCGGAAACCTTACTTA 955
Db 911 GCGCCGCAAGCGGTGAGCATGTGTATTCGATGCAACCGGAAACCTTACTTA 970
Oy 956 CCCTTGACATGATGAGCAATTTTCTAGAGATAGATTAGTG-CTTGGGAAAGCTAACAG 1014
Db 971 CTCTTGACATGAGCAATTTTCTAGAGATAGATTAGTGCTTGGGAACTTGGAGACAG 1030
Oy 1015 GTGCTGATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
Db 1031 GTGCTGATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
Oy 1075 GCAACCTTGCTATTAATTCGATCA--TTTGTGGGCACTTAAATGAGTCCGGT 1132
Db 1091 GCAACCTTGCTATTAATTCGATCA--TTTGTGGGCACTTAAATGAGTCCGGT 1150
Oy 1133 ACAAACCGGAGAGGAGGAGTGAAGTCAAGTCCCTGAGGCTTATGGGAGGCTTC 1192
Db 1151 ACAAACCGGAGAGGAGGAGTGAAGTCAAGTCCCTGAGGCTTATGGGAGGCTTC 1210
Oy 1193 ACACGTATATACATGCGCGCTACAGAGGCTTCCAAACCGGAGGAGGCTTATCTGAG 1252
Db 1211 ACACGTGCTACATGCGCGCTACAGAGGCTTCCAAACCGGAGGAGGCTTATCTGAG 1270
Oy 1253 AAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1312
Db 1271 AAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1330
Oy 1313 GTATTCGCGATCGCATGTCGCGGCTGAATCGTTCCGGGCTTGTACACACCGCGCT 1372
Db 1331 GTATTCGATGATCGAATGCTACGCTGAATCGTTCCGGGCTTGTACACACCGCGCT 1390
Oy 1373 CACACATGAGAGTGGTTCACAGAGCAAGTATTAACCGTAAAGAGAGGCGCTTGC 1432
Db 1391 CACACATGAGAGTGGTTCACAGAGCAAGTATTAACCGTAAAGAGAGGCGCTTGC 1450
Oy 1433 CACGCTGATTCATGACTGGGGTG 1457
Db 1451 CACTTGTGATTCATGACTGGGGTG 1475

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RESULT 12
US-10-831-286A-48671
; Sequence 48671, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, OIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001

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; CURRENT APPLICATION NUMBER: US/10/831.286A
; CURRENT FILING DATE: 2004-04-25
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48671
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Citrobacter youngae
US-10-831-286A-48671

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Query Match 69.2%; Score 1008.4; DB 9; Length 1530;
Best Local Similarity 82.4%; Pred. No. 2,66-305;
Matches 1206; Conservative 0; Mismatches 251; Indels 7; Gaps 4;

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Oy 1 ATTGAACGCTGCGCGCAATGCTTTACATGCAATGCAACGCGACGACGATGCTTG--- 57
Db 22 ATTGAACGCTGCGCGCAATGCTTTACATGCAATGCAACGCGACGACGATGCTTG 81
Oy 58 -CATCTGCTGCGAGTGGCGGACCGGTGATGATGCAATCGGAACGTATCCAGAAAGGG 116
Db 82 TCCTTGGGTGACGATGCGCGACCGGTGATGATGCAATCGGAACGTATCCAGAAAGGG 141
Oy 117 GGTAAACGATGAGAAAGATGATGCTAATACCGCATATCTTAAGAGAGGAAACAGGGGATC 176
Db 142 GATTAACGATGAGAAACGATGATGATGCTAATACCGCATATCTTAAGAGAGGAAACAGGGGATC 201
Oy 177 GAAAGACCTTGGCGCTTTTGGAGCGCGCATGCTGATTAAGTATGCTGCTGCTGCTGCTG 236
Db 202 TTGGGCGCTTGGCGCTTTTGGAGCGCGCATGCTGATTAAGTATGCTGCTGCTGCTGCTG 261
Oy 237 CTACCAAGGCGACATGATGATGCTGCTGAGAGAGACCAAGCACTCTGAGCTGGA 296
Db 262 TCACCTAGGCGACATGATGCTGCTGCTGAGAGAGACCAAGCACTCTGAGCTGGA 321
Oy 297 CACGAGCGACATCTCTACGAGGAGGACAGTGGGGAATTTTGGCAATGGGCGCAAGCT 356
Db 322 CACGAGCGACATCTCTACGAGGAGGACAGTGGGGAATTTTGGCAATGGGCGCAAGCT 381
Oy 357 GATCAGCAATGCGCGCTGAGTGAAGAGGCTTGGGCTTGAAGCTTTTCACTGAG 416
Db 382 GATCAGCAATGCGCGCTGAGTGAAGAGGCTTGGGCTTGAAGCTTTTCACTGAG 441
Oy 417 AAGAAAGCTTACGCTTAATATGCTGATCTGATGACGCTATCCAGCAAGAAAGACCGGC 476
Db 442 AAGAAAGCTTACGCTTAATATGCTGATCTGATGACGCTATCCAGCAAGAAAGACCGGC 501
Oy 477 TAACTAGTGCAGACGCGCGGTAAATAGTAAAGGAGTCAAGCGTTAATCGAATTAATCTGG 536
Db 502 TAACTAGTGCAGACGCGCGGTAAATAGTAAAGGAGTCAAGCGTTAATCGAATTAATCTGG 561
Oy 537 GCGTAAAGGATGCGCAGCGCGCTTGTGAATGATGTAATCCCGGCTTAACTG 596
Db 562 GCGTAAAGGATGCGCAGCGCGCTTGTGAATGATGTAATCCCGGCTTAACTG 621
Oy 597 GAATTCGTTGAACTCAAGCTAGAGTGTGACAGAGGAGTGAATTCATGTGTA 656
Db 622 GAATTCGTTGAACTCAAGCTAGAGTGTGACAGAGGAGTGAATTCATGTGTA 681
Oy 657 GCAATGAAATGCGAAGATATGAGAAACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 716
Db 682 GCAATGAAATGCGAAGATATGAGAAACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 741
Oy 717 CACTGACGCTCATGACGAAAGCGTGGGAGCAACAGATTAATGATACCTTGGTATGCTCA 776
Db 742 GACTGACGCTCATGACGAAAGCGTGGGAGCAACAGATTAATGATACCTTGGTATGCTCA 801
Oy 777 GCGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 835
Db 802 GCGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 861
Oy 836 CGTGAAGTTACCGCTGGGAGTACGCTGCAAGATTAAACTCAAGAAATTGACGG 895

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Db 862 CGTTAAGTCACCGCCCTGGGAGTAACGCGCAAGTTAAACCTCAATGATTTAGCGG 921
Qy 896 GACCCGCAAGCGGTGATTAATGTGATTAATTCATGCAACGCAAAAACTTAACTTA 955
Db 922 GGGCCGCAAGCGGTGATTAATGTGATTAATTCATGCAACGCAAAAACTTAACTTA 981
Qy 956 CCCTTGACATGTAGCGAATTTCTAGAGATTAATGTC-CTTCGGAAAGCTAAACAG 1014
Db 982 CTCCTTGACATTCAGAGAACTTAGAGATGCTTGGTGCCTTCGGAACTTCAGACAG 1041
Qy 1015 GTCTGCAATGCTGTCTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1074
Db 1042 GTCTGCAATGCTGTCTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1101
Qy 1075 GCAACCTTGATTAATTCATTC-ATTGTTGGGCACTTTAATGACCTGCGGTGA 1133
Db 1102 GCAACCTTATCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1161
Qy 1134 CAACCGGAGAAAGTGGGAGTACGTCAGTCTCTCATGCTCTTATGAGGCTTCA 1193
Db 1162 TAAACTGAGAAAGTGGGAGTACGTCAGTCTCTCATGCTCTTATGAGGCTTCA 1221
Qy 1194 CAGGTATACAGTGGGAGTACGTCAGTCTCTCATGCTCTTATGAGGCTTCA 1253
Db 1222 CAGGTATACAGTGGGAGTACGTCAGTCTCTCATGCTCTTATGAGGCTTCA 1281
Qy 1254 AAGCGCTGCTAGTCCGAGTCTGCACTGCACTCCGTAAGTCCGATCCGATG 1313
Db 1282 AAGCGCTGCTAGTCCGAGTCTGCACTGCACTCCGTAAGTCCGATCCGATG 1341
Qy 1314 TAAATCGGATCAGATGTGCGGTGAATACCTCCGCTTGTATACACACCGCGTGC 1373
Db 1342 TAAATCGGATCAGAAATGCCAGTGTGAATACCTCCGCTTGTATACACACCGCGTGC 1401
Qy 1374 ACACCAAGGAGTGGGTTTCCAGAAAGAGTGTCTAACCGTAAGAGGCGCTTGGC 1433
Db 1402 ACACCAAGGAGTGGGTTTCCAGAAAGAGTGTCTAACCGTAAGAGGCGCTTGGC 1461
Qy 1434 ACGGTGAGTATCAGCTGAGGCTG 1457
Db 1462 ACTTGTGATTCATGACTGGGCTG 1485

RESULT 13
US-10-831-286A-48686
; Sequence 48686, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDESS, DARRIEL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831, 286A
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48686
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Yokenella regensburgei
US-10-831-286A-48686

Query Match 69.1%; Score 1007.2; DB 9; Length 1492;
Best Local Similarity 82.4%; Pred. No. 6,2e-305;
Matches 1204; Conservative 0; Mismatches 253; Indels 5; Gaps 4;
Qy 1 ATTGAACGCTGCGGATGCTTACATGCAAGTCAAGCAAGCAAGCAAGTGTGAT 60

Db 1 ATTGAACGCTGCGGATGCTTACATGCAAGTCAAGCAAGCAAGCAAGTGTGATGCT 60
Qy 61 CT--GGTGGAGATGCGGAGCGGTGATGATGATCGAAACSTATTCAGAAAGGGGG 118
Db 61 CTGGGGTGAAGATGCGGAGCGGTGATGATGATCGAAACSTATTCAGAAAGGGGG 120
Qy 119 TAAAGCATGAAAGATGCTAATACCGATATACCTAAGAGGAAAGAGGGGATGCA 178
Db 121 TAACTGTAAGACGCTGATTAATACCGATATACCTAAGAGGAAAGAGGGGATGCA 180
Qy 179 AAGACCTTGGGCTTTTGAAGCGGCGCATGCTGATTAAGTATGTTGGGTAAAGGCTT 238
Db 181 CGGCGCTTGGGCTTTTGAAGCGGCGCATGCTGATTAAGTATGTTGGGTAAAGGCTT 240
Qy 239 ACCAAGCGACGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 298
Db 241 ACCAAGCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy 299 CGGCGGAGATCTCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 358
Db 301 CGGCGGAGATCTCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 359 TCGAGCAATGCGCGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 418
Db 361 TCGAGCAATGCGCGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 419 GAAAGGTTACGTTAATTAATGCTGATCAAGCGGATTCAGCAAGAAAGCAAGCGCTA 478
Db 421 GAAGCGATCGGTTAATTAATGCTGATCAAGCGGATTCAGCAAGAAAGCAAGCGCTA 480
Qy 479 ACTACGTCAGAGAGCGCGGTAAATGATAGGTTGAAGGTTAATGATGATGATGATGAT 538
Db 481 ACTACGTCAGAGAGCGCGGTAAATGATAGGTTGAAGGTTAATGATGATGATGATGAT 540
Qy 539 GTAAGGGTGCAGAGCGGCTTTGTAAGTCAATGTAATTCGCGGCTTAACTTGGGA 598
Db 541 GTAAGGGTGCAGAGCGGCTTTGTAAGTCAATGTAATTCGCGGCTTAACTTGGGA 600
Qy 599 ATTGCGTTGAATCTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 658
Db 601 ACTGCAATTCGAACTGGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
Qy 659 AGTGAATGCTGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAG 718
Db 661 GGTGAATGCTGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAG 720
Qy 719 CTGACGCTGATGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAG 778
Db 721 CTGACGCTGATGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAG 780
Qy 779 CCCTAAACGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAGGAG 837
Db 781 CCCTAAACGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAGGAG 840
Qy 838 TGAAGTGAACCGGCTGGGAGTACGCTGCAAGATTAATTAATTAATTAATTAATTAAT 897
Db 841 TGAAGTGAACCGGCTGGGAGTACGCTGCAAGATTAATTAATTAATTAATTAATTAAT 900
Qy 898 CCGGCAAGCGGTGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAGGAG 957
Db 901 CCGGCAAGCGGTGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAGGAG 960
Qy 958 CTGACATGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAG 1016
Db 961 CTGACATGATGATTAATGAAAGCAATTCGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Qy 1017 GCTGCAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076
Db 1021 GCTGCAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1077 AACCTTGTCTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135

Dh 1081 AACCTTATCTTTGTCACAGCGTTGCGCGGGAACTCAAAGGAGATGCACTGATTA 1140
Qy 1136 AACCGAGAGAGGCGGATGACGTCAGTCTCTATGCGCCTTATGGTATGGGCTTCA 1195
Db 1141 AACCGAGAGAGGCGGATGACGTCAGTCTCTATGCGCCTTATGGTATGGGCTTCA 1200
Qy 1196 CGTATACAAATGCGCGGATGACAGAGGTTGCCAACCGGAGGGGAGCTTAATCTCAAAA 1255
Db 1201 CGTCTACAAATGCGCGGATGACAGAGGTTGCCAACCGGAGGGGAGCTTAATTA 1260
Qy 1256 GCGCGTCTAGTCCGAGATCGAGTCTGCACTCGATCGATCGAAATCGTACTA 1315
Db 1261 GTATGTCTAGTCCGAGATCGAGTCTGCACTCGATCGATCGAAATCGTACTA 1320
Qy 1316 ATGCGGATGACGATGTCGCGGATGATACGTTCCCGGCTTGTATCAACCGCCCTGAC 1375
Db 1321 ATCTGATGATGAAATGACAGCGTGAATACGTTCCCGGCTTGTATCAACCGCCCTGAC 1380
Qy 1376 ACCATGGAAGTGGGTTTCAACGAGAGAGTACTAACCGTAAAGAGGCGCTTGCCAC 1435
Db 1381 ACCATGGAAGTGGGTTTCAACGAGAGAGTACTAACCGTAAAGAGGCGCTTGCCAC 1440
Qy 1436 GGTGAGATTGATGATCGGCGTG 1457
Db 1441 TTTGTGATTGATGATCGGCGTG 1462

RESULT 14
US-10-831-286A-48687
; Sequence 48687, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHIDRESS, DARRELL
; TITLE OR INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831, 286A
; PRIOR FILING DATE: 2004-04-26
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 48687
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: *Yokenella regensburgei*
US-10-831-286A-48687

Query Match 69.1%; Score 1007.2; DB 9; Length 1519;
Best Local Similarity 82.4%; Pred. No. 6.2e-305;
Matches 1204; Conservative 0; Mismatches 253; Indels 5; Gaps 4;

Qy 1 ATTGAAGCTGCGCGCATGCTTTACATGCAATGCCAGACGAGATGCTTGCAT 60
Db 22 ATTGAAGCTGCGCGCATGCTTTACATGCAATGCCAGACGAGATGCTTGCAT 81
Qy 61 CT--GGTGGCGAGTGGCGGAGCGGAGTGAATGATCGAAGCTATCGAAGAGGGGG 118
Db 82 CTGGGGTGAAGAGTGGCGGAGCGGAGTGAATGATGCTGGAAGTGGCGGAGAGGG 141
Qy 119 TAAAGCATGAAAGATGCTTAATACCGCATATACCTTAAGAGAGAAAGAGGGATCGA 178
Db 142 TAAAGCATGAAAGATGCTTAATACCGCATATACCTTAAGAGAGAAAGAGGGATCGA 201
Qy 179 AAGAGCTTGGCTTTTGAAGCGCGGAGTGTGATGATGATGATGATGATGATGATGAT 238
Db 202 CGGGCTCTTGGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 261
Qy 239 ACCAAGCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 298

Dh 262 ACCTAGGCGAGCATCCCTAGCTGCTTGAAGATGACAGGACACATGAACTGAGACA 321
Qy 299 CGGCGGAGATCTCTACCGGAGAGCGAGTGGGGAATTTTGAACAATGGGCGGAGCTTGA 358
Db 322 CGGTCAGATCTCTACCGGAGAGCGAGTGGGGAATTTTGAACAATGGGCGGAGCTTGA 381
Qy 359 TCCAGCATGCGCGGATGAGTGAAGAGGCTTCCGGTTGTAAAGCTCTTTCAGTCAAGAA 418
Db 382 TCGAGCATGCGCGGATGAGTGAAGAGGCTTCCGGTTGTAAAGCTCTTTCAGTCAAGAG 441
Qy 419 GAAAGGATGAGGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478
Db 442 GAAAGGATGAGGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 501
Qy 479 ACTAGTCCAGAGCGCGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 538
Db 502 ACTCGGCGAGAGCGCGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 561
Qy 539 GTAAAGGATGAGGAGGCGGCTTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 598
Db 562 GTAAAGGATGAGGAGGCGGCTTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 621
Qy 599 ATGCGTTTGAATCTACAGGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
Db 622 ACTGATTCGAAATGAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
Qy 659 AGTGAATGCGTGAAGATTAAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 718
Db 682 GGTGAATGCGTGAAGATTAAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 741
Qy 719 CTGACGCTCAGTACAGAAAGCGTGGGAGGAAACAGGATTAATGATGATGATGATGATGATGATGAT 778
Db 742 CTGACGCTCAGTACAGAAAGCGTGGGAGGAAACAGGATTAATGATGATGATGATGATGATGATGAT 801
Qy 779 CCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
Db 802 CCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
Qy 838 TGAAGTGAACCGCTGGGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
Db 862 TGAAGTGAACCGCTGGGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 921
Qy 898 CCGGCAAGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
Db 922 CCGGCAAGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 981
Qy 958 CTGACATGAT 1016
Db 982 CTGACATGAT 1041
Qy 1017 GCTGATGCT 1076
Db 1042 GCTGATGCT 1101
Qy 1077 AACCTTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
Db 1102 AACCTTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1161
Qy 1136 AACCGAGAGAGTGGGAGTGAAGTCAAGTCTCATAGCCTTATGAGGTAGGGCTTCA 1195
Db 1162 AACCGAGAGAGTGGGAGTGAAGTCAAGTCTCATAGCCTTATGAGGTAGGGCTTCA 1221
Qy 1196 CGTATACAAATGCGCGGATGACAGAGGTTGCCAACCGGAGGGGAGCTTAATCTCAAGAA 1255
Db 1222 CGTCTACAAATGCGCGGATGACAGAGGTTGCCAACCGGAGGGGAGCTTAATTA 1281
Qy 1256 GCGCGTCTAGTCCGAGATCGAGTCTGCACTCGTGAAGTCCGATGATGATGATGATGATGATGAT 1315
Db 1282 GTATGTCTAGTCCGAGATCGAGTCTGCACTCGTGAAGTCCGATGATGATGATGATGATGATGAT 1341
Qy 1316 ATGCGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1375
Db 1342 ATGCGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1401

QY	1436	GGTGAAGATCTCACTGGGGGTG	1457
QY	1376	ACCATGGGAAGGGGTTTACACAGAAAGCAGTAGTCTAACCGTAAGAGAGGGGCTTGGCAC	1435
Db	1402	ACCATGGGAAGGGGTTTGCAGAAAGTAGTAGCTTAACCTTCGGGAGAGGGGCTTACAC	1461
QY	1462	TTTGTGATCTACAGACTGGGGTGG	1483
Db			

RESULT 15
US-10-831

```

Sequence 48675, Application US/10831286A
Publication No. US20060046246A1
GENERAL INFORMATION:
APPLICANT: ZENG, QIANDONG
APPLICANT: CHATELIER, SONIA
APPLICANT: MOIR, DONALD T.
APPLICANT: LACROIX, BRUNA
APPLICANT: CHILDRESS, DARRELL
TITLE OF INVENTION: GENES, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
FILE REFERENCE: 032796-174.001
CURRENT APPLICATION NUMBER: US/10/831.286A
CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: 60/464,955
PRIOR FILING DATE: 2003-04-24
NUMBER OF SEQ ID NOS: 48788
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48675
LENGTH: 1495
TYPE: DNA
ORGANISM: Proteus penneri
US-10-831-286A-48675

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Query Match	69.0%	Score 1005.4	BD 9	Length 1495
Best Local Similarity	82.7%	Pred. No. 2.3e-304		
Matches 121	Conservative	0	Mismatches 246	Indels 8
				Gaps 5

Qy	1	TTGAAGCGCTGGGGGCGCATGCTTTACACATGCAAGTCGAAACGGAGAC--GGATGCTTGC	58
Db	1	ATTGAACGCTGGGGGGCGGCGCTTAACAATGCAAGTCGAGCGGTAAAGAAAGAGCTTTC	60
Qy	59	AT--CTGGTGGCGAGTGGCGGAACGGGTGAAGTAATGATCGGAACCTATCCAGAAAGGGG	116
Db	61	TTTCTTGCTGACGAGCGGGCGGGAACGGGTGAAGTAATGATGGGATCTGCCGATAGGGGG	120
Qy	117	GGTAACGCAATCGAAAGATGTGCTAAATACCGCAATATCTCTAAGAGAGAAAGCAAGGGATC	176
Db	121	GATTAATCACTAGGAACCGGTGGCTAAATACCGCAATGACGTCTACCGAACCAAGCAGGGGGCTTC	180
Qy	177	GAAAGACCTTGGCGCTTTTGGAGCGGCGCATGTCTGATTGACTAGTGTGGGTAAAGGC	236
Db	181	TTTGGAGCTTGGCGCTATCGGATGAACCCATATGGAGATTAGTAGTGAAGTGAAGGTAAGGC	240
Qy	237	CTACCAAGCGGAGCATGATAGTTGGTCTGAGAGACACACACCACTGGGACTGAGA	296
Db	241	TCACTAGGGGAGAGATCTTAGCGTGTGAGAGAGATGATCAAGCCACACTGGGACTGAGA	300
Qy	297	CACGGCCACAGACTCTACCGGGAGGACAGTAGTGGGAAATTTTGGACAATGGGCGCAAGCCT	356
Db	301	CACGGCCCAACATCTCTACGGGAGGACAGCATGGGGAAATATGGACAATGGGCGCAAGCCT	360
Qy	357	GATCCAGCAATGCCCGCTGAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTCACTCGAG	416
Db	361	GATGACAGCCATGCGCGGTATGAAGAAAGCCCTTAAGGTTGTAAAGTACTTTTCAAGCGGGG	420
Qy	417	AAGAAAGGTTACGGTAAATATCGTGACTCATGACGGTATCGACAGAAAGAACACCGGC	476
Db	421	AGGAAGGTGATTAAGTTAATTAATCACTTTATGCAATTGAGCTTAAACCGGAGAAAGACACCGGC	480
Qy	477	TAACTAGTTCACAGACCGCCGGTAATACGTACGGTTCGAAAGCTTAAATCGGAATTAATCTGG	536
Db	481	TAACTCGTCCAGACAGCGCGGTAAATACGAAGGTGCAAGCGCTTAATCGGAATTAATCTGG	540

OY	537	GCCTAAAGGGGTGCGACGGCGGCTTTTGAAGTCAGAAATGTAATCCCGGGCTTAACTGCG	536
Db	541	GCCTAAAGCCACGCGACGGCGCTCAATTAAAGTCAGATGTAAACCCCGAGCTTAACTTGG	600
OY	597	GAATTGCGTTTGAATCAACAGGCTTGAAGTGTGGCAGAGGGAGGTGGAAATTCATGTGTGA	656
Db	601	GAATTGCATCTGAACACTGGTTGGCTTGAAGCTCTTGTAGAGGGGGGTAGAAATTCATGTGTGA	660
OY	657	GCAGTGAAGAAGCGTATGATATGGAAGAAACATGAGTGGGGAAGGAGCGCTCCGGGTAA	716
Db	661	GCGGTGAAGAAGCGTATGAGATGTGAGAGAAATCCGGTGGCGAAGGCGGCCCCCTGGACAAA	720
OY	717	CACGTAGCGCTCATGSCAGAAAGCGTGGGAGCAAAACAGATTATGATACCTCTGGTATGTCA	776
Db	721	GACTGAGCGCTCAGGTGCGAAAGCGTGGGAGCAAAACAGATTATGATACCTCTGGTATGTCCA	780
OY	777	CGCGCTTAAACGATGTC-AACTAGTTGTGGGCTTATTAAGCTTGGTAAAGAACTTACG	835
Db	781	CGCGTAAACGATGTGCAATTTAAGGTTGTGGTCTTGAACCGGTGCTTGGAGAGCTTACG	840
OY	836	CGTGAAGTTAACCGCTCTGGGGAGTACGGTTCGCAAGATTAAACTCAAAAGGAATTGACGGG	895
Db	841	CGTTAAATCGACCGCTCGGGAGTACGGCGCAAGGTTTAAACTCAATATTAATTTGACGGG	900
OY	896	GACCCGCAACAAGCGGTGAGATTATGTGATTAATTCATGCAACGCAAAAACCTTACTTA	955
Db	901	GCGCCGCAACAAGCGGTGAGCAATGTGGTTTAATTCATGCAACGCGAAAGAACTTACTTA	960
OY	956	CCCTTGCATGTAGCGAATTTCTTGAAGATAGTATAGTG-CTTTCGGAAAGCTTACACAG	1014
Db	961	CTCTTGCATCTCAGCAATCTTTTGAAGATAGAGAGTGTCTTCGGGAAAGCTGAGACAG	1020
OY	1015	GTCCTGATAGGCTGTGTGACGTCGTGTGTGTGAGATGGTGGGTTAAGTCCCGCAACGAGC	1074
Db	1021	GTCGTGATAGGCTGTGTGACGTCGTGTGTGTGAAATGTGGTTAAGTCCCGCAACGAGC	1080
OY	1075	GCAACCCCTTGCATTAATTGCCATCATTTTG--GTTGGGCACTTTAAATGAGACTGCGGTG	1132
Db	1081	GCAACCCCTTATCCTTTGTTCGCCAGCCCGTATAGGCGGAACTCAAAAGAGACTGCGGCTG	1140
OY	1133	ACAAAACCGAGGAAGGTGGGGATGAGCTCAAGTCTCATGAGCCCTTATGAGTAGGCGCTTC	1192
Db	1141	ATTAACCGGAGGAAGGTGGGGATGAGCTCAAGTCAATGATCATGAGCCCTTACGAGTAGGCGCTAC	1200
OY	1193	ACACGTATATCAATGTGCGGCTACAGAGGGGTGTGCCAACCCGCGAGGGGAGCTTATCTCAG	1252
Db	1201	ACACGTGCTTCAATATGCGAGTAAAMAAGAAAGGACCTCGCGAGCAACACGGAACTCAT	1260
OY	1253	AAAGCGGTGTGTATGTCGCGAGTCGGAAGTCTGCAACTGCACTCCGTGAAGTCCGAATCGCTA	1312
Db	1261	AAAGTCTGTGTATGTCGCGAGTTGGAATCTTGCAACTGCACTCCATGAAGTCCGAATCGCTA	1320
OY	1313	GTAATCGCGATCAGCATGTCCGCGTGAATACGTTTCCCGGGTCTTGTACACACGCCCGGT	1372
Db	1321	GTAATGCTATATCAAGATGCTACGGTGAATATGCTTCCCGGGCTTGTACACACGCCCGGT	1380
OY	1373	CACACCATGGGAGTGGGTTTACACCAAGACAGGTATCTTACCCGTAAAGAGGGCGCTTGC	1432
Db	1381	CACACCATGGGAGTGGGTTTGCAAAAMAAGTATAGTACTTAACTTTCGGGAGGGCGCTTAC	1440
OY	1433	CACGGTGAATTCATGACTGGGGTG 1457	
Db	1441	CACCTTGTGATTCATGACTGGGGTG 1465	

Search completed: April 6, 2006, 21:46:35
Job time : 731 secs

Db 181 GACCTTCCGCTTTTGGAGCGCCGATGCTGATTAGTATGATGAGGTAAGGCTTAC 240
 Qy 241 CAAGGCGAGATCAGTATGTTGTTCTGAGAGACGACGACACCTGGAGCTGAGACAG 300
 Db 241 CAAGGCGAGATCAGTATGTTGTTCTGAGAGACGACGACACCTGGAGCTGAGACAG 300
 Qy 301 GCCCAAGCTCTTACGGGAGGACAGATGGGGAAATTTTGGACATTTGGGCGGAAACCTGATC 360
 Db 301 GCCCAAGCTCTTACGGGAGGACAGATGGGGAAATTTTGGACATTTGGGCGGAAACCTGATC 360
 Qy 361 CAGCAATGCCGCTGAGTGAAGAAGGCTTCCGATTGTAAAGCTCTTTCAGTGAAGAGA 420
 Db 361 CAGCAATGCCGCTGAGTGAAGAAGGCTTCCGATTGTAAAGCTCTTTCAGTGAAGAGA 420
 Qy 421 AAAGGTTACGGTAATATATGTTGATCTCATGACGGTATCGACAGAAAGACCGGCTTAC 480
 Db 421 AAAGGTTACGGTAATATATGTTGATCTCATGACGGTATCGACAGAAAGACCGGCTTAC 480
 Qy 481 TACGTCCAGACGACCGCGGTAAATCGTAAAGGCTCAAGCTTAACTCGGAATTCGGGCGT 540
 Db 481 TACGTCCAGACGACCGCGGTAAATCGTAAAGGCTCAAGCTTAACTCGGAATTCGGGCGT 540
 Qy 541 AAAGGTTACGGTAATATATGTTGATCTCATGACGGTATCGACAGAAAGACCGGCTTAC 600
 Db 541 AAAGGTTACGGTAATATATGTTGATCTCATGACGGTATCGACAGAAAGACCGGCTTAC 600
 Qy 601 TGGCTTTGAAACTACAGGCTTAAAGTGTGACAGAGGAGGTGAAATTCATGTGTAGCAG 660
 Db 601 TGGCTTTGAAACTACAGGCTTAAAGTGTGACAGAGGAGGTGAAATTCATGTGTAGCAG 660
 Qy 661 TGAATGCGGTAGATGTGAAAGAACTCATGTGCGAAAGGACGCTCTGGTTAACTACT 720
 Db 661 TGAATGCGGTAGATGTGAAAGAACTCATGTGCGAAAGGACGCTCTGGTTAACTACT 720
 Qy 721 GACGCTCATSCAGAAAGCGTGGGAGCAAAACAGATTAAATCCCTGTAGTCCAGGCC 780
 Db 721 GACGCTCATSCAGAAAGCGTGGGAGCAAAACAGATTAAATCCCTGTAGTCCAGGCC 780
 Qy 781 CTAAACGATGTCAACTAGTGTGGGCTTATTAAGGCTTGTAAACGAACTTAAAGCGCTGA 840
 Db 781 CTAAACGATGTCAACTAGTGTGGGCTTATTAAGGCTTGTAAACGAACTTAAAGCGCTGA 840
 Qy 841 AGTTGACCGGCTGGGAGTACGCTGCGAAGATTAAACCTAAAGGAATTGACGGGAGGCC 900
 Db 841 AGTTGACCGGCTGGGAGTACGCTGCGAAGATTAAACCTAAAGGAATTGACGGGAGGCC 900
 Qy 901 GCAAGACGGGTGATTAATGATTAATTCGATGCAACGCGAAACCTTACCTACCTT 960
 Db 901 GCAAGACGGGTGATTAATGATTAATTCGATGCAACGCGAAACCTTACCTACCTT 960
 Qy 961 GACATGTAAGCAATTTTCTAGAGATAGATTAGTCTTCCGGAACGCTTACACAGTCTG 1020
 Db 961 GACATGTAAGCAATTTTCTAGAGATAGATTAGTCTTCCGGAACGCTTACACAGTCTG 1020
 Qy 1021 CATGGCTGTGTCAAGCTGCTGTGTGATGATGTTAGTCCCGGAAGAGCGCAACC 1080
 Db 1021 CATGGCTGTGTCAAGCTGCTGTGTGATGATGTTAGTCCCGGAAGAGCGCAACC 1080
 Qy 1081 CTTGTCTTAATTTGCAATCTTGGTGTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140
 Db 1081 CTTGTCTTAATTTGCAATCTTGGTGTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140
 Qy 1141 GAGAAAGTGGGAGTGAAGTCAAGTCTCATGAGGCTTATGGTGAAGGCTTCAACGTTAA 1200
 Db 1141 GAGAAAGTGGGAGTGAAGTCAAGTCTCATGAGGCTTATGGTGAAGGCTTCAACGTTAA 1200
 Qy 1201 TAAATGCGCGGTGACAGAGGTTGCCAACCCGGAAGGAGGAGCTTAACTGAGAAAGCGG 1260
 Db 1201 TAAATGCGCGGTGACAGAGGTTGCCAACCCGGAAGGAGGAGCTTAACTGAGAAAGCGG 1260
 Qy 1261 TCGTAGTCCGAGTCCGAGTGTGCAACTGACTCGGTGAAGTGGGAATCGGTAGTAATCGC 1320
 Db 1261 TCGTAGTCCGAGTCCGAGTGTGCAACTGACTCGGTGAAGTGGGAATCGGTAGTAATCGC 1320

Qy 1321 GGATCAGCATGTCCGGGTGAATACGTTCCCGGGCTTTGTACACACCGCCGTCACACAT 1380
 Db 1321 GGATCAGCATGTCCGGGTGAATACGTTCCCGGGCTTTGTACACACCGCCGTCACACAT 1380
 Qy 1381 GGAAGTGGGTTTACACAGAGAGAGTGTCTAACCTGAAGAGGCGCTTGGCAGCGTGA 1440
 Db 1381 GGAAGTGGGTTTACACAGAGAGAGTGTCTAACCTGAAGAGGCGCTTGGCAGCGTGA 1440
 Qy 1441 GATTCATGACTGGGGTG 1457
 Db 1441 GATTCATGACTGGGGTG 1457
 RESULT 2
 US-10-659-980A-1
 ; Sequence 1, Application US/10659980A
 ; Publication No. US20040106133A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hovaneq, Timothy A
 ; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
 ; FILE REFERENCE: 81289-284781
 ; CURRENT APPLICATION NUMBER: US/10/659,980A
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: US 09/573,684
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 60/386,217
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,218
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,219
 ; PRIOR FILING DATE: 2002-09-19
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 1457
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; OTHER INFORMATION: AOB Type A R7clone140 16S rDNA
 US-10-659-980A-1
 Query Match 100.0%; Score 1457; DB 7; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTTGAACGCTGGCGGATGCTTTAACAATGAAAGTGAACGCGACGAGATGCTTGCAT 60
 Db 1 ATTTGAACGCTGGCGGATGCTTTAACAATGAAAGTGAACGCGACGAGATGCTTGCAT 60
 Qy 61 CTGTGGCGAGTGGCGGAGCGGCTGAGTATGCAATGCGAAAGTATCCAGAAAGAGGGGGTA 120
 Db 61 CTGTGGCGAGTGGCGGAGCGGCTGAGTATGCAATGCGAAAGTATCCAGAAAGAGGGGGTA 120
 Qy 121 AGGCATCGAAAGATGCTAATACCGCATATCTAAGAGAGAAAGAGGGGATCGAAA 180
 Db 121 AGGCATCGAAAGATGCTAATACCGCATATCTAAGAGAGAAAGAGGGGATCGAAA 180
 Qy 181 GACCTTGCCTTTTGGAGCGGCGGATGTCTGATTAGTGAAGTGTGGGTAAGAGGCTTAC 240
 Db 181 GACCTTGCCTTTTGGAGCGGCGGATGTCTGATTAGTGAAGTGTGGGTAAGAGGCTTAC 240
 Qy 241 CAAGGCGAGATCAGTATGTTGTTGAGAGGACGACACGCACTGGGACTGAGACAG 300
 Db 241 CAAGGCGAGATCAGTATGTTGTTGAGAGGACGACACGCACTGGGACTGAGACAG 300
 Qy 301 GCCCAGACTCTTACCGGAGGAGCAGAGTGGGAAATTTTGGACATGGGCGCAAGCTGATC 360
 Db 301 GCCCAGACTCTTACCGGAGGAGCAGAGTGGGAAATTTTGGACATGGGCGCAAGCTGATC 360
 Qy 361 CAGCAATGCCGCTGAGTGAAGAAGGCTTCCGATTGTAAAGCTCTTTCAGTGAAGAGA 420
 Db 361 CAGCAATGCCGCTGAGTGAAGAAGGCTTCCGATTGTAAAGCTCTTTCAGTGAAGAGA 420

421 AAAGTTACGGTAATTAATCGTACTCATGACGGTATGACAGAGAACGACCGGCTAAC 480
 421 AAAGTTACGGTAATTAATCGTACTCATGACGGTATGACAGAGAACGACCGGCTAAC 480
 481 TACGTCCAGACAGCCCGGCTTAATCGTGGGTGACAGGGTTAATGGAATTACTGGGGGT 540
 481 TACGTCCAGACAGCCCGGCTTAATCGTGGGTGACAGGGTTAATGGAATTACTGGGGGT 540
 541 AAAGGTGCGCAGCGCGCTTTGTAAAGTCAAGATGTGAAATCCCGGGCTTTAACTGGGAAT 600
 541 AAAGGTGCGCAGCGCGCTTTGTAAAGTCAAGATGTGAAATCCCGGGCTTTAACTGGGAAT 600
 601 TGGCTTTGAAACTACAGAGCTAGAGTGTGCGCAGAGGGAGTGAATTCACATGTGACAG 660
 601 TGGCTTTGAAACTACAGAGCTAGAGTGTGCGCAGAGGGAGTGAATTCACATGTGACAG 660
 661 TGAATGGGTAGAGTATGAAAGAACATGATGGGAGAGCGCTCCGGGTTAACT 720
 661 TGAATGGGTAGAGTATGAAAGAACATGATGGGAGAGCGCTCCGGGTTAACT 720
 721 GACGCTCATGACAGAAACGGTGGGAGCAACAGATTAGATACCTGGTATGACAGCGC 780
 721 GACGCTCATGACAGAAACGGTGGGAGCAACAGATTAGATACCTGGTATGACAGCGC 780
 781 CTAAACGATGCTACTAGTGTGGGCTTATTAAGCTTTGTTGTAACGAACTAACCGCTGA 840
 781 CTAAACGATGCTACTAGTGTGGGCTTATTAAGCTTTGTTGTAACGAACTAACCGCTGA 840
 841 AGTTGACCGGCTGGGAGTACCGGTGCAAGATTAACTCAAGAAATTGACGGGAGCC 900
 841 AGTTGACCGGCTGGGAGTACCGGTGCAAGATTAACTCAAGAAATTGACGGGAGCC 900
 901 GCAAGAGCGTGGATTAATGTGATTAATTCAGATGCAACGCAAAACCTTACCTTACCCTT 960
 901 GCAAGAGCGTGGATTAATGTGATTAATTCAGATGCAACGCAAAACCTTACCTTACCCTT 960
 961 GACATGTAAGCAATTTTCTAGATAGATTAAGTGTGGGAAACCTTAACTTAACTGCTG 1020
 961 GACATGTAAGCAATTTTCTAGATAGATTAAGTGTGGGAAACCTTAACTTAACTGCTG 1020
 1021 CATGCTGTGCTGACGCTGTGCTGAGATGTTGGGTTAAGTCCGCAACGAGCGCAAC 1080
 1021 CATGCTGTGCTGACGCTGTGCTGAGATGTTGGGTTAAGTCCGCAACGAGCGCAAC 1080
 1081 CTGTGATTAATGTCATATTTGGTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140
 1081 CTGTGATTAATGTCATATTTGGTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140
 1141 GAGGAAGGTGGAGATGACGTCAAGTCTTCAATGAGGCTTAAAGGCTTCAACGTTAA 1200
 1141 GAGGAAGGTGGAGATGACGTCAAGTCTTCAATGAGGCTTAAAGGCTTCAACGTTAA 1200
 1201 TACATGCGCGGTACAGAGGCTTGGCAACCGCGAGGGGAGCTAATCTCAAGAAAGCGG 1260
 1201 TACATGCGCGGTACAGAGGCTTGGCAACCGCGAGGGGAGCTAATCTCAAGAAAGCGG 1260
 1261 TCGTAGTCCGATCGGATGCTGCAACTGCACTCGGTGAAGTGGAAATGCTAATGATGCG 1320
 1261 TCGTAGTCCGATCGGATGCTGCAACTGCACTCGGTGAAGTGGAAATGCTAATGATGCG 1320
 1321 GGATCAGATGTCGCGGTGAATACGTTCCGGGTCTTGTACACACCGCGCTTCAACAT 1380
 1321 GGATCAGATGTCGCGGTGAATACGTTCCGGGTCTTGTACACACCGCGCTTCAACAT 1380
 1381 GGGAGTGGTTTCAACAGAGAGGTAGCTTAACTGTAAGAGAGGGGCGCTTGCACAGGTGA 1440
 1381 GGGAGTGGTTTCAACAGAGAGGTAGCTTAACTGTAAGAGAGGGGCGCTTGCACAGGTGA 1440
 1441 GATTATGACTGGGGTG 1457
 1441 GATTATGACTGGGGTG 1457

RESULT 3
 US-10-659-983A-1
 ; Sequence 1, Application US/10659983A
 ; Publication No. US20040157313A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hovaneq, Timothy A
 ; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
 ; FILE REFERENCE: 81289-28479
 ; CURRENT APPLICATION NUMBER: US/10/659, 983A
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: US 09/573,684
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 60/386,217
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,218
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,219
 ; PRIOR FILING DATE: 2002-09-19
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 1
 ; LENGTH: 1457
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: MOB Type A R7clonel40 16S rDNA
 US-10-659-983A-1
 Query Match 100.0%; Score 1457; DB 7; Length 1457;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGAAAGCGTGGGCGCATGCTTTACATGCAATGCAAGCGGACGACGATGCTTGCAT 60
 1 ATGAAAGCGTGGGCGCATGCTTTACATGCAATGCAAGCGGACGACGATGCTTGCAT 60
 61 CTGTGGGCGAGTGGCGGACGGGTGATGCAATGCAAGCGGACGACGATGCTTGCAT 120
 61 CTGTGGGCGAGTGGCGGACGGGTGATGCAATGCAAGCGGACGACGATGCTTGCAT 120
 121 AGCATGCAAGATGCTGTAATACCGCATATATCTTAAAGAGAAAGCGGAGATCGAAA 180
 121 AGCATGCAAGATGCTGTAATACCGCATATATCTTAAAGAGAAAGCGGAGATCGAAA 180
 181 GACCTTGGCTTTTGAAGCGGCGCATGCTGATTAAGTGTGGGTTAAAGCTTAC 240
 181 GACCTTGGCTTTTGAAGCGGCGCATGCTGATTAAGTGTGGGTTAAAGCTTAC 240
 241 CAAGCGCATGCTGATGCTGTAATACCGCATATATCTTAAAGAGAAAGCGGAGATCGAAA 300
 241 CAAGCGCATGCTGATGCTGTAATACCGCATATATCTTAAAGAGAAAGCGGAGATCGAAA 300
 301 GCCAGACTCTTACGGGAGGAGCAGATGAGGAAATTTTGAACATGAGGCGCAAGCTGATC 360
 301 GCCAGACTCTTACGGGAGGAGCAGATGAGGAAATTTTGAACATGAGGCGCAAGCTGATC 360
 361 CAGCAATGCGCGTGAAGTGAAGAAAGGCTTGGGTTGAAAGCTTTCACTGAGAAAGA 420
 361 CAGCAATGCGCGTGAAGTGAAGAAAGGCTTGGGTTGAAAGCTTTCACTGAGAAAGA 420
 421 AAAGTTACGGTAATTAATCGTACTCATGACGGTATGACAGAGAACGACCGGCTAAC 480
 421 AAAGTTACGGTAATTAATCGTACTCATGACGGTATGACAGAGAACGACCGGCTAAC 480
 481 TACGTCCAGACAGCCCGGCTTAATCGTGGGTGACAGGGTTAATGGAATTACTGGGGGT 540
 481 TACGTCCAGACAGCCCGGCTTAATCGTGGGTGACAGGGTTAATGGAATTACTGGGGGT 540
 541 AAAGGTGCGCAGCGCGCTTTGTAAAGTCAAGATGTGAAATCCCGGGCTTTAACTGGGAAT 600
 541 AAAGGTGCGCAGCGCGCTTTGTAAAGTCAAGATGTGAAATCCCGGGCTTTAACTGGGAAT 600

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QY 601 TGGCTTGAACCTACAGGCTAGAGTGTGGCAAGAGGAGGTAATTCATGCTACAG 660
DB 601 TGGCTTGAACCTACAGGCTAGAGTGTGGCAAGAGGAGGTAATTCATGCTACAG 660
QY 661 TGAATGCTAGAGATATGGAAGAACTGCAATGCGAGGAGGCTCTGGGTTAACT 720
DB 661 TGAATGCTAGAGATATGGAAGAACTGCAATGCGAGGAGGCTCTGGGTTAACT 720
QY 721 GAGGCTCATGCAAGAAAGCTGGGAGCAAAAGATTAGATCCTGATGTCACGCC 780
DB 721 GAGGCTCATGCAAGAAAGCTGGGAGCAAAAGATTAGATCCTGATGTCACGCC 780
QY 781 CTAAAGATGCTCAACTAGTGTGGGCTTATAGGCTTGTTAGTAAAGGCTAACGGGTGA 840
DB 781 CTAAAGATGCTCAACTAGTGTGGGCTTATAGGCTTGTTAGTAAAGGCTAACGGGTGA 840
QY 841 AGTTGACCCGCTGGGAGTACGCTCGCAAGATTAACTCAAAAGAAATTAACGGGAGCC 900
DB 841 AGTTGACCCGCTGGGAGTACGCTCGCAAGATTAACTCAAAAGAAATTAACGGGAGCC 900
QY 901 GCAAAAGCGGTGATTAATGATTAATTCGATGCAACGGGAAAACCTTACCTACCTT 960
DB 901 GCAAAAGCGGTGATTAATGATTAATTCGATGCAACGGGAAAACCTTACCTACCTT 960
QY 961 GACATGATGGAATTTCTAGAGATAGATAGTCTCGGGAACGGCTAACAGAGTGTG 1020
DB 961 GACATGATGGAATTTCTAGAGATAGATAGTCTCGGGAACGGCTAACAGAGTGTG 1020
QY 1021 CATGCTGTGCTAGCTGCTGTGCTGATGATGTTGGGTTAAGTCCCGCAAGAGGCAAC 1080
DB 1021 CATGCTGTGCTAGCTGCTGTGCTGATGATGTTGGGTTAAGTCCCGCAAGAGGCAAC 1080
QY 1081 CTGTGCTAATTAATGCTCACTATTTGTTGGGCACTTTAATGAGACTGCGGTGA 1140
DB 1081 CTGTGCTAATTAATGCTCACTATTTGTTGGGCACTTTAATGAGACTGCGGTGA 1140
QY 1141 GAGGAGGTTGGGATGAGCTGCTCATGCGCTTATGGGATGGGCTTCAACAGTAA 1200
DB 1141 GAGGAGGTTGGGATGAGCTGCTCATGCGCTTATGGGATGGGCTTCAACAGTAA 1200
QY 1201 TACAATGCGCGCTACAGAGGTTGCCAACCGGAGGAGGAGCTTAATCTGAGAAAGCG 1260
DB 1201 TACAATGCGCGCTACAGAGGTTGCCAACCGGAGGAGGAGCTTAATCTGAGAAAGCG 1260
QY 1261 TCGTATGCTGCGATGCGAGTGTGCACTCGCTGTAAGTCCGATCGCTAGTATCGC 1320
DB 1261 TCGTATGCTGCGATGCGAGTGTGCACTCGCTGTAAGTCCGATCGCTAGTATCGC 1320
QY 1321 GATTCAGCATGTCGCGGTGAATCGTTCCGGGCTTGTACACACCGCGCTACACCAT 1380
DB 1321 GATTCAGCATGTCGCGGTGAATCGTTCCGGGCTTGTGTACACACCGCGCTACACCAT 1380
QY 1381 GGGAGTGGGTTTACAGAGAGCAAGTATTAACCGTAAGAGAGGCGCTTGCACGGTGA 1440
DB 1381 GGGAGTGGGTTTACAGAGAGCAAGTATTAACCGTAAGAGAGGCGCTTGCACGGTGA 1440
QY 1441 GATTCACTGAGGAGTG 1457
DB 1441 GATTCACTGAGGAGTG 1457

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; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA
US-10-659-948a-2

Query Match 99.7%; Score 1452.2; DB 7; Length 1457;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATTGAACGCTGGCGCATGCTTTACATGCAAGTGAACGGCAGACGGATCTGCAT 60
DB 1 ATTGAACGCTGGCGCATGCTTTACATGCAAGTGAACGGCAGACGGATCTGCAT 60
QY 61 CTGGTGCGAGTGGCGGAGCGGAGTGAATGCAATGCAAGGATCCAGAAAGAGGGGGA 120
DB 61 CTGGTGCGAGTGGCGGAGCGGAGTGAATGCAATGCAAGGATCCAGAAAGAGGGGGA 120
QY 121 AGCATGGAAGATGCTAATATCCGATATATCTTAAGAGAGAAAGAGGGATGAAA 180
DB 121 AGCATGGAAGATGCTAATATCCGATATATCTTAAGAGAGAAAGAGGGATGAAA 180
QY 181 GACCTTGGCTTTGGAGCGGCCGATGCTGATTAAGTGAATGTTGGGTTAAAGGCTTAC 240
DB 181 GACCTTGGCTTTGGAGCGGCCGATGCTGATTAAGTGAATGTTGGGTTAAAGGCTTAC 240
QY 241 CAAGGAGAGATCAGATGTTGTTGAGAGAGAGACACACACACTGGGACTGAGACAG 300
DB 241 CAAGGAGAGATCAGATGTTGTTGAGAGAGAGACACACACACTGGGACTGAGACAG 300
QY 301 GCCCAGACTCTTACGGGAGGAGCAGTGGGGAATTTGGACAATGGGCGCAAGCTGATC 360
DB 301 GCCCAGACTCTTACGGGAGGAGCAGTGGGGAATTTGGACAATGGGCGCAAGCTGATC 360
QY 361 CAGCAATGCGCGGTGAGTGAAGAGGCGCTTCCGTTGTAAAGCTCTTTCAGTCGAGAGA 420
DB 361 CAGCAATGCGCGGTGAGTGAAGAGGCGCTTCCGTTGTAAAGCTCTTTCAGTCGAGAGA 420
QY 421 AAAGGTTAGGTAATTAATCGTGAATGATGAGGATGAGAGGATGAGAGAGACACCGCTAAC 480
DB 421 AAAGGTTAGGTAATTAATCGTGAATGATGAGGATGAGAGGATGAGAGAGACACCGCTAAC 480
QY 481 TACGTGCGAGCAGCGCGGTAATTAAGTGGGTGCAAGCTTAACTGGAATTAAGTGGGCGT 540
DB 481 TACGTGCGAGCAGCGCGGTAATTAAGTGGGTGCAAGCTTAACTGGAATTAAGTGGGCGT 540
QY 541 AAAGGTCGCGAGCGGCTTTGTAAGTCAAGTGAATCCCGGCTTAACCTGGGAAT 600
DB 541 AAAGGTCGCGAGCGGCTTTGTAAGTCAAGTGAATCCCGGCTTAACCTGGGAAT 600
QY 601 TGGCTTGAACCTACAGGCTAGAGTGTGGCAAGAGGAGGTAATTCATGCTACAG 660
DB 601 TGGCTTGAACCTACAGGCTAGAGTGTGGCAAGAGGAGGTAATTCATGCTACAG 660
QY 661 TGAATGCTAGAGATATGGAAGAACTGCAATGCGAGGAGGCTCTGGGTTAACT 720
DB 661 TGAATGCTAGAGATATGGAAGAACTGCAATGCGAGGAGGCTCTGGGTTAACT 720
QY 721 GAGGCTCATGCAAGAAAGCTGGGAGCAAAAGATTAGATCCTGATGTCACGCC 780
DB 721 GAGGCTCATGCAAGAAAGCTGGGAGCAAAAGATTAGATCCTGATGTCACGCC 780
QY 781 CTAAAGATGCTCAACTAGTGTGGGCTTATAGGCTTGTTAGTAAAGGCTAACGGGTGA 840
DB 781 CTAAAGATGCTCAACTAGTGTGGGCTTATAGGCTTGTTAGTAAAGGCTAACGGGTGA 840

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RESULT 4
US-10-659-948a-2
; Sequence 2, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovance, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19

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Db      781 CTAACGATGTCACTAATGTTGGGCTTATAGGCTTGGTAAGAACTAACCGCTGA 840
Qy      841 AGTGAACCGCTGGGAGTACGCTGCAAGATTAACTCAAGGAATTGACGGGACCC 900
Db      841 AGTGAACCGCTGGGAGTACGCTGCAAGATTAACTCAAGGAATTGACGGGACCC 900
Qy      901 GCACAAAGCGGTGATTAATGTGATTAATTCATGCAAGCGGAAAACTTACCTT 960
Db      901 GCACAAAGCGGTGATTAATGTGATTAATTCATGCAAGCGGAAAACTTACCTT 960
Qy      961 GACATGTAGCGAATTTCTAGAGATAGATTAGTCTGGGAAAGCTAACAGGTGCTG 1020
Db      961 GACATGTAGCGAATTTCTAGAGATAGATTAGTCTGGGAAAGCTAACAGGTGCTG 1020
Qy      1021 CATGGCTGTCTGACGCTGTCTGAGATGTTGGGTTAAGTCCGCAACGACGCAAC 1080
Db      1021 CATGGCTGTCTGACGCTGTCTGAGATGTTGGGTTAAGTCCGCAACGACGCAAC 1080
Qy      1081 CTTGTCAATTAATTCATCAATTTTGGTGGGCACTTTAATGAGACTGCGGATGACAA 1140
Db      1081 CTTGTCAATTAATTCATCAATTTTGGTGGGCACTTTAATGAGACTGCGGATGACAA 1140
Qy      1141 GAGAGAGGTGGGAGATGAGTCAAGTCTCATAGCCCTTATGGGTAGGGCTTACAGCT 1200
Db      1141 GAGAGAGGTGGGAGATGAGTCAAGTCTCATAGCCCTTATGGGTAGGGCTTACAGCT 1200
Qy      1201 TACAATGCGCGCTACAGAGGTTGCAACCCGCGAGGGGAGCTAATCTCAAGAAAGCCG 1260
Db      1201 TACAATGCGCGCTACAGAGGTTGCAACCCGCGAGGGGAGCTAATCTCAAGAAAGCCG 1260
Qy      1261 TCGTAGTCCGATCGGAATCTGCAACTGACTCCGTTGAAGTGGAAATGCTAATGCT 1320
Db      1261 TCGTAGTCCGATCGGAATCTGCAACTGACTCCGTTGAAGTGGAAATGCTAATGCT 1320
Qy      1321 GGATCAGCATGTCGCGGTGAATAGCTTCCGGGCTTGTGACACACCGCCCTCAACCAT 1380
Db      1321 GGATCAGCATGTCGCGGTGAATAGCTTCCGGGCTTGTGACACACCGCCCTCAACCAT 1380
Qy      1381 GGGAGTGGGTTTCAACGAAGAGGTAAGTCTAACCGTAAGAGAGGCGCTTGGCAAGTGA 1440
Db      1381 GGGAGTGGGTTTCAACGAAGAGGTAAGTCTAACCGTAAGAGAGGCGCTTGGCAAGTGA 1440
Qy      1441 GATTCATGACTGGGGGTG 1457
Db      1441 GATTCATGACTGGGGGTG 1457

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RESULT 5
US-10-659-980A-2

Sequence 2, Application US/10659980A
Publication No. US20040106133A1

GENERAL INFORMATION:

APPLICANT: Hovanec, Timothy A

TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria

FILE REFERENCE: 81289-284781

CURRENT APPLICATION NUMBER: US/10/659,980A

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: US 09/573,684

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: US 60/386,217

PRIOR FILING DATE: 2002-09-19

PRIOR APPLICATION NUMBER: US 60/386,218

PRIOR FILING DATE: 2002-09-19

PRIOR APPLICATION NUMBER: US 60/386,219

PRIOR FILING DATE: 2002-09-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 1457

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA
US-10-659-980A-2

Query Match 99.7%; Score 1452.2; DB 7; Length 1457;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATTGAAGCGTGGGGGCAATGCTTTACATGCAATGCAAGCGGACGAGTGTGTCAT 60
Db      1 ATTGAAGCGTGGGGGCAATGCTTTACATGCAATGCAAGCGGACGAGTGTGTCAT 60
Qy      61 CTGTGGCGAGTGGCGGACGCGGTGATGATGATGCAATGCAAGCTATCCAGAAAGGGGGT 120
Db      61 CTGTGGCGAGTGGCGGACGCGGTGATGATGATGCAATGCAAGCTATCCAGAAAGGGGGT 120
Qy      121 ACGCATGAAAGATGTGCTAATACCGCATATCTTAAAGAGAAAGCAGGAGATCGAAA 180
Db      121 ACGCATGAAAGATGTGCTAATACCGCATATCTTAAAGAGAAAGCAGGAGATCGAAA 180
Qy      181 GACCTTGCGCTTTTGGAGCGGCGGATGCTGATTAGTGTGGGTAAAGGCTTAC 240
Db      181 GACCTTGCGCTTTTGGAGCGGCGGATGCTGATTAGTGTGGGTAAAGGCTTAC 240
Qy      241 CAAGCGACGATCAGTAGTGTCTGAGAGGACGACGACCACTGGACTGAGACAG 300
Db      241 CAAGCGACGATCAGTAGTGTCTGAGAGGACGACGACCACTGGACTGAGACAG 300
Qy      301 GCCCAGACTCTTACGGAGGAGCAGAGTGGGGAATTTTGGACAAATGGGCGCAAGCTGAT 360
Db      301 GCCCAGACTCTTACGGAGGAGCAGAGTGGGGAATTTTGGACAAATGGGCGCAAGCTGAT 360
Qy      361 CAGCAATGCGCGGTGATGAAAGGCTTGGGTGTAAGCTTCACTCGAAGAGA 420
Db      361 CAGCAATGCGCGGTGATGAAAGGCTTGGGTGTAAGCTTCACTCGAAGAGA 420
Qy      421 AAAGTTACGGTAAATATCGTGAATGATGATGATGATGATGATGATGATGATGAT 480
Db      421 AAAGTTACGGTAAATATCGTGAATGATGATGATGATGATGATGATGATGATGAT 480
Qy      481 TACGTCCAGAGCGCGGCTAATGATGATGATGATGATGATGATGATGATGATGAT 540
Db      481 TACGTCCAGAGCGCGGCTAATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy      541 AAAGGTGCGGAGCGGCTTGTAAAGTGAATGATGATGATGATGATGATGATGAT 600
Db      541 AAAGGTGCGGAGCGGCTTGTAAAGTGAATGATGATGATGATGATGATGATGAT 600
Qy      601 TGGCTTGAATCTCAAGGCTAGAGTGGGAGAGGAGGAGTGAATCCCGGGCTTAACCTGG 660
Db      601 TGGCTTGAATCTCAAGGCTAGAGTGGGAGAGGAGGAGTGAATCCCGGGCTTAACCTGG 660
Qy      661 TGAATGCTAGATATGGAAGAAATGATGATGATGATGATGATGATGATGATGAT 720
Db      661 TGAATGCTAGATATGGAAGAAATGATGATGATGATGATGATGATGATGATGAT 720
Qy      721 GACGCTATGCAAGAAAGCGTGGGAGCAACAGATTAATCCCTGATGATGATGAT 780
Db      721 GACGCTATGCAAGAAAGCGTGGGAGCAACAGATTAATCCCTGATGATGATGATGAT 780
Qy      781 CTAACGATGCACTAGTGTGGGCTTATGAGTGTGATGATGATGATGATGATGAT 840
Db      781 CTAACGATGCACTAGTGTGGGCTTATGAGTGTGATGATGATGATGATGATGAT 840
Qy      841 AGTGAACCGCTGGGAGTACGCTGCAAGATTAACTCAAGGAATTGACGGGACCC 900
Db      841 AGTGAACCGCTGGGAGTACGCTGCAAGATTAACTCAAGGAATTGACGGGACCC 900
Qy      901 GCACAAAGCGGTGATTAATGTGATTAATTCATGCAAGCGGAAAACTTACCTT 960
Db      901 GCACAAAGCGGTGATTAATGTGATTAATTCATGCAAGCGGAAAACTTACCTT 960
Qy      961 GACATGTAGCGAATTTCTAGAGATAGATTAGTCTGGGAAAGCTAACAGGTGCTG 1020

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QY 1201 TACATGCGCGGTACAGAGGTTGCAACCCGCCAGGAGGAGCTAATCTCAGAAAGCGCG 1260
DB 1201 TACAAATGCGCGGTACAGAGGTTGCAACCCGCCAGGAGGAGCTAATCTCAGAAAGCGCG 1260
QY 1261 TCGAGTCCGGAATGGAAGTCTGCAACTGCACTCCGCTGGAAGTCCGGAATGCTAGTAAATCGC 1320
DB 1261 TCGAGTCCGGAATGGAAGTCTGCAACTGCACTCCGCTGGAAGTCCGGAATGCTAGTAAATCGC 1320
QY 1321 GGATCAGCATCTCCGCTGGAATGCACTCCGCTGTTTACACACCCGCCGCTCAACCAT 1380
DB 1321 GGATCAGCATCTCCGCTGGAATGCACTCCGCTGTTTACACACCCGCCGCTCAACCAT 1380
QY 1381 GGAAGTGGCTTTCACAGAGAGAGTACTCTAACCTTAAGAGAGGCGCTTCCACCGTGA 1440
DB 1381 GGAAGTGGCTTTCACAGAGAGAGTACTCTAACCTTAAGAGAGGCGCTTCCACCGTGA 1440
QY 1441 GATTGATGACTGGGGTG 1457
DB 1441 GATTGATGACTGGGGTG 1457

RESULT 7
US-10-659-948A-20
Sequence 20, Application US/10659948A
Publication No. US20040101946A1
GENERAL INFORMATION:
APPLICANT: Hovaneq, Timothy A
TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-294309
CURRENT APPLICATION NUMBER: US/10/659,948A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US 09/573,684
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/386,217
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,218
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,219
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 1491
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: N. aestuarii-like AOB B16clone57 16S rDNA
US-10-659-948A-20

Query Match 95.5%; Score 1391.6; DB 7; Length 1491;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 301 GCCAGACTCTACGGGAGGAGCAGAGTGGGAAATTTTGAACAATGGGCGCAAGCTGATC 360
DB 318 GCCAGACTCTACGGGAGGAGCAGAGTGGGAAATTTTGAACAATGGGCGCAAGCTGATC 377
QY 361 CAGCAATGCGCGGTGAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTCACTGAGAGA 420
DB 378 CAGCAATGCGCGGTGAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTCACTGAGAGA 437
QY 421 AAGGTTACGGTAATTAATGTAAGTATGATGACGGTATGACAGAAAGAACCCGGCTAAC 480
DB 438 AAGGTTACGGTAATTAATGTAAGTATGATGACGGTATGACAGAAAGAACCCGGCTAAC 497
QY 481 TAGGTGACACAGCGCGGTAAATACGTAAGGAGTGAAGCTTAATCGGAATTAATGAGCGT 540
DB 498 TAGGTGACACAGCGCGGTAAATACGTAAGGAGTGAAGCTTAATCGGAATTAATGAGCGT 557
QY 541 AAGGAGTGCAGAGCGCGCTTGTAGTACAGATGGAATCCCGGGCTTAACCTGGAGAT 600
DB 558 AAGGAGTGCAGAGCGCGCTTGTAGTACAGATGGAATCCCGGGCTTAACCTGGAGAT 617
QY 601 TCGGTTGAAAATTAAGGCTTAAGTGTGCAAGAGGAGTGAATTCATGTGTAGCAG 660
DB 618 TCGGTTGAAAATTAAGGCTTAAGTGTGCAAGAGGAGTGAATTCATGTGTAGCAG 677
QY 661 TGAATTCGCTAGAGATTAAGAGAACTGATGGCGGAAGCAGCGCTGGGTTAACT 720
DB 678 TGAATTCGCTAGAGATTAAGAGAACTGATGGCGGAAGCAGCGCTGGGTTAACT 737
QY 721 GAGGCTATGACAGAAAGCGTGGGAGCAAAACAGATTAGTAACTCTGTAGTACAGCC 780
DB 738 GAGGCTATGACAGAAAGCGTGGGAGCAAAACAGATTAGTAACTCTGTAGTACAGCC 797
QY 781 CTAAACAGATGCAACTAGTGTGGGCTTAATAGCTTGTGTAACGAAGCTAACGCGTGA 840
DB 798 CTAAACAGATGCAACTAGTGTGGGCTTAATAGCTTGTGTAACGAAGCTAACGCGTGA 857
QY 841 AGTTGACCGGCTGGGAGTACCGTCCGCAAGATTAAACCTAAAGGAATTGACGGGAGCC 900
DB 858 AGTTGACCGGCTGGGAGTACCGTCCGCAAGATTAAACCTAAAGGAATTGACGGGAGCC 917
QY 901 GCACAGCGGTGAGTAAATGATGATTAATTCGATGCAACCGGAAACCTTAACCTACCTT 960
DB 918 GCACAGCGGTGAGTAAATGATGATTAATTCGATGCAACCGGAAACCTTAACCTACCTT 977
QY 961 GACATGTAGCGAATTTCTAGATAGATTAGTG-CTTCGGGAGCGCTAACACAGTGCT 1019
DB 978 GACATGTAGCGAATTTCTAGATAGATTAGTG-CTTCGGGAGCGCTAACACAGTGCT 1037
QY 1020 GCATGCTGTGCTGACGCTGCTGCTGCTGAGATGTTGGGTTAAAGTCCGCCAAGAGCGGAAAC 1079
DB 1038 GCATGCTGTGCTGACGCTGCTGCTGCTGAGATGTTGGGTTAAAGTCCGCCAAGAGCGGAAAC 1097
QY 1080 CTTGTGATTAATTCGATCATATTGTTGGGCACTTAATGAGAGTCCGGTGAACAAC 1139
DB 1098 CTTGTGATTAATTCGATCATATTGTTGGGCACTTAATGAGAGTCCGGTGAACAAC 1157
QY 1140 GAGAGAGTGGGAGTACGCTCAAGTCTCATGGCCCTTAATGGGTAGGGCTTCAACAGTA 1199
DB 1158 GAGAGAGTGGGAGTACGCTCAAGTCTCATGGCCCTTAATGGGTAGGGCTTCAACAGTA 1217
QY 1200 ATACAAATGCGCGGTACAGAGGTTGCCAACCCCGAGGGGAGGTAATTCAGAAACCGC 1259
DB 1218 ATACAAATGCGCGGTACAGAGGTTGCCAACCCCGAGGGGAGGTAATTCAGAAACCGC 1277
QY 1260 GTGCTAGTCCGGAATGGAAGTCTGCAACTCCGTAAGTGGGTAATTCGTAATTCG 1319
DB 1278 GTGCTAGTCCGGAATGGAAGTCTGCAACTCCGTAAGTGGGTAATTCGTAATTCG 1337
QY 1320 CGGATCAGCATGTCGCGGTAAATCGTCCCGGCTTGTACACACCGCGCTACACCA 1379
DB 1338 CGGATCAGCATGTCGCGGTAAATCGTCCCGGCTTGTGTACACACCGCGCTACACCA 1397

QY 1380 TGGAGTGGTTTCAACGAGAGGATGATCTAACCTTAAGAGAGGGCTTGGCAAGG 1439
 DB 1398 TGGAGTGGTTTCAACGAGAGGATGATCTAACCTTAAGAGAGGGCTTGGCAAGG 1457
 QY 1440 AGATTCACTGAGGGG 1457
 DB 1458 AGATTCACTGAGGGG 1475

RESULT 8

US-10-659-980A-20
 ; Sequence 20, Application US/10659980A
 ; Publication No. US20040106133A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hovane, Timothy A
 ; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
 ; FILE REFERENCE: 81289-284781
 ; CURRENT APPLICATION NUMBER: US/10/659,980A
 ; CURRENT FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: US 09/573,684
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 60/386,217
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,218
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,219
 ; PRIOR FILING DATE: 2002-09-19
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 20
 ; LENGTH: 1491
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: N. Aestuarii-like AOB Bf16c1one57 16S rDNA
 US-10-659-980A-20

Query Match 95.5%; Score 1391.6; DB 7; Length 1491;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATGGAACGCTGGGCGGATGCTTTACACATGCAAGTCCAAAGCGAGCGAGTGGCAT 60
 DB 18 ATTGAACGCTGGGCGGATGCTTTACACATGCAAGTCCAAAGCGAGCGAGTGGCAT 77
 QY 61 CTGTGGCGAGTGGCGGAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 120
 DB 78 CTGTGGCGAGTGGCGGAGCGGATGATGATGATGATGATGATGATGATGATGATGAT 137
 QY 121 AGCGATCGAAGATGCTTAATACCGCATTAATCTTAAGAGAGAGAGAGAGAGAGAG 180
 DB 138 ACCCATCGAAGATGCTTAATACCGCATTAATCTTAAGAGAGAGAGAGAGAGAGAG 197
 QY 181 GACCTTGCGCTTTTGAAGCGGCGAGTGTGATTAAGTGTGATTAAGTGTGATTAAGT 240
 DB 198 GACCTTGCGCTTTTGAAGCGGCGAGTGTGATTAAGTGTGATTAAGTGTGATTAAGT 257
 QY 241 CAAGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 258 CAAGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
 QY 301 GCCCAACTCTTAACGAG 360
 DB 318 GCCCAACTCTTAACGAG 377
 QY 361 CAGCAATGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 378 CAGCAATGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 437
 QY 421 AAAGTTACGGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 438 AAAGTTACGGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497

QY 481 TACGTCCAGACGCGCGGTAATTAAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 498 TACGTCCAGACGCGCGGTAATTAAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
 QY 541 AAAGGTGGCGAGCGGCTTTTGAAGTCAAGATGATGATGATGATGATGATGATGATGAT 600
 DB 558 AAAGGTGGCGAGCGGCTTTTGAAGTCAAGATGATGATGATGATGATGATGATGATGAT 617
 QY 601 TCGCTTTGAACCTAACAGGCTTAAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 618 TCGCTTTGAACCTAACAGGCTTAAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
 QY 661 TGAATGCGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 678 TGAATGCGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
 QY 721 GAGCTCATGACGAAAGCGTGGGAGCAAGAGATTAAGTATGATGATGATGATGATGATGAT 780
 DB 738 GAGCTCATGACGAAAGCGTGGGAGCAAGAGATTAAGTATGATGATGATGATGATGATGAT 797
 QY 781 CTAAACGATGCTAAGTGTGCTGGGCTTTATGAGCTTGTAAAGAGAGAGAGAGAGAG 840
 DB 798 CTAAACGATGCTAAGTGTGCTGGGCTTTATGAGCTTGTAAAGAGAGAGAGAGAGAG 857
 QY 841 AGTTGACCGGCTGGGAGATGAGTGGCAAGATTAAGTAAAGAGAGAGAGAGAGAGAG 900
 DB 858 AGTTGACCGGCTGGGAGATGAGTGGCAAGATTAAGTAAAGAGAGAGAGAGAGAGAG 917
 QY 901 GACAAGCGGCTGATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 960
 DB 918 GACAAGCGGCTGATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 977
 QY 961 GACATGATGAGATTTTCTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1019
 DB 978 GACATGATGAGATTTTCTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1037
 QY 1020 GCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
 DB 1038 GCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097
 QY 1080 CCTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
 DB 1098 CCTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1157
 QY 1140 GGAAGAGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
 DB 1158 GGAAGAGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
 QY 1200 ATACAATGCGGCTGACAGAGGCTGCAACCGCGAGGAGAGAGAGAGAGAGAGAGAG 1259
 DB 1218 ATACAATGCGGCTGACAGAGGCTGCAACCGCGAGGAGAGAGAGAGAGAGAGAGAG 1277
 QY 1260 GTCTGATGCTCGAGTGGAGTCTGCAACTGCACTGCTGAGTGGAGTGGAGTGGAGT 1319
 DB 1278 GTCTGATGCTCGAGTGGAGTCTGCAACTGCACTGCTGAGTGGAGTGGAGTGGAGT 1337
 QY 1320 CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1379
 DB 1338 CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1397
 QY 1380 TGGAGTGGGTTTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1439
 DB 1398 TGGAGTGGGTTTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1457
 QY 1440 AGATTCACTGAGGGG 1457
 DB 1458 AGATTCACTGAGGGG 1475

RESULT 9
 US-10-659-983A-20
 ; Sequence 20, Application US/10659983A
 ; Publication No. US20040157313A1


```

GENERAL INFORMATION:
APPLICANT: Hovanec, Timothy A
TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-28479
CURRENT APPLICATION NUMBER: US/10/659,983A
PRIORITY FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: US 09/573,684
PRIORITY FILING DATE: 2000-05-19
PRIORITY APPLICATION NUMBER: US 60/386,217
PRIORITY FILING DATE: 2002-09-19
PRIORITY APPLICATION NUMBER: US 60/386,218
PRIORITY FILING DATE: 2002-09-19
PRIORITY APPLICATION NUMBER: US 60/386,219
PRIORITY FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 1491
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: N. Aestuarii-like AOB Bf1clone57 16S rDNA
US-10-659-983A-20

Query Match      95.5%; Score 1391.6; DB 7; Length 1491;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

OY 1 ATTGAAGCTGGCGGCGCATGCTTTACACATGCAAGTCGAACGGGACACGGAATGCTTGAT 60
DB 18 ATTGAAGCTGGCGGCGCATGCTTTACACATGCAAGTCGAACGGGACACGGAATGCTTGAT 77
OY 61 CTGGTGGCGAGTGGCGGACGAGGTGATATGATCGAATCGAATCGAAGAGGGGGGTA 120
DB 78 CTGGTGGCGAGTGGCGGACGAGGTGATATGATCGAATCGAATCGAAGAGGGGGGTA 137
OY 121 ACGCATCGAAGATGTGCTAATACCGCATATCTCTAAGAGAGAAAGCGGGATCGAAA 180
DB 138 ACGCATCGAAGATGTGCTAATACCGCATATCTCTAAGAGAGAAAGCGGGATCGAAA 197
OY 181 GACCTGCTGCTTTTGGAGCGGCGCATGCTGATGATGATGATGATGATGATGATGATGAT 240
DB 198 GACCTGCTGCTTTTGGAGCGGCGCATGCTGATGATGATGATGATGATGATGATGATGAT 257
OY 241 CAAGCGCATGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 258 CAAGCGCATGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
OY 301 GCCCAACTCTTACCGGAGGACGAGTGGGGAATTTTGGACATGAGGCGCAAGCTGATC 360
DB 318 GCCCAACTCTTACCGGAGGACGAGTGGGGAATTTTGGACATGAGGCGCAAGCTGATC 377
OY 361 CAGCAATGCCCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 378 CAGCAATGCCCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
OY 421 AAAGTTACGGTAAATATCGTCACTCATGACGATGATGACAGAGAGAGAGAGAGAGAGAG 480
DB 438 AAAGTTACGGTAAATATCGTCACTCATGACGATGATGACAGAGAGAGAGAGAGAGAGAG 497
OY 481 TACGTCAGACGACCGCGGTAAATCGTAAAGGTCAGAGCTTAATCGAATTCGAGCGT 540
DB 498 TACGTCAGACGACCGCGGTAAATCGTAAAGGTCAGAGCTTAATCGAATTCGAGCGT 557
OY 541 AAAGGTCGCGAGCGGCTTTTGTAGTCAATGTAATTCCTCCGCGCTTAACCTGGGAT 600
DB 558 AAAGGTCGCGAGCGGCTTTTGTAGTCAATGTAATTCCTCCGCGCTTAACCTGGGAT 617
OY 601 TCGCTTTGAAATCTAAGAGCTAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 618 TCGCTTTGAAATCTAAGAGCTAGAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
OY 661 TGAATTCGTAGATATGGAAGAAATCATGATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 720

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DB 678 TGAATTCGTAGATATGGAAGAAATCATGATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 737
OY 721 GAGCTCATGACGAAAGCGTGGGAGCAAAACAGATTAAATCCTGTAGTCAAGCGC 780
DB 738 GAGCTCATGACGAAAGCGTGGGAGCAAAACAGATTAAATCCTGTAGTCAAGCGC 797
OY 781 CTAACGATGTCATGATGTTGGGCTTTATAGCTTGTGTAACGAAAGCTTAAGCGGTA 840
DB 798 CTAACGATGTCATGATGTTGGGCTTTATAGCTTGTGTAACGATGTAACGCGTGA 857
OY 841 AGTTGACCGCTGGGAGTACCGGTGCAAGATTAACTCAAGAGATTGACGGGAGCC 900
DB 858 AGTTGACCGCTGGGAGTACCGGTGCAAGATTAACTCAAGAGATTGACGGGAGCC 917
OY 901 GCACACGCGTGTATATGATGATTAATTCGATGCAACGCGAAACCTTAACCTTACCTT 960
DB 918 GCACACGCGTGTATATGATGATTAATTCGATGCAACGCGAAACCTTAACCTTACCTT 977
OY 961 GACATGAGGGAATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
DB 978 GACATGAGGGAATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1037
OY 1020 GCATGCGCTGCTGAGCTCGGTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1079
DB 1038 GCATGCGCTGCTGAGCTCGGTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1097
OY 1080 CTTGTGATTAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
DB 1098 CTTGTGATTAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1157
OY 1140 GAGAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
DB 1158 GAGAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
OY 1200 ATCAATGCGCGCGTACAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGAT 1259
DB 1218 ATCAATGCGCGCGTACAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGAT 1277
OY 1260 GTCTGATGCGGATGCGAGTCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAAT 1319
DB 1278 GTCTGATGCGGATGCGAGTCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAAT 1337
OY 1320 CGGATCAGATGTCGCGGTGAATCGTCCCGGCTCTTGTACACACCGCCGCTACACCA 1379
DB 1338 CGGATCAGATGTCGCGGTGAATCGTCCCGGCTCTTGTACACACCGCCGCTACACCA 1397
OY 1380 TGGGAGTGGGCTTACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1439
DB 1398 TGGGAGTGGGCTTACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1457
OY 1440 AGATTGATGACTGGGCTG 1457
DB 1458 AGATTGATGACTGGGCTG 1475

RESULT 10
US-10-659-948A-19
Sequence 19, Application US/10659948A
Publication No. US20040101946A1
GENERAL INFORMATION:
APPLICANT: Hovanec, Timothy A
TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-294309
CURRENT APPLICATION NUMBER: US/10/659,948A
PRIORITY FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: US 09/573,684
PRIORITY FILING DATE: 2000-05-19
PRIORITY APPLICATION NUMBER: US 60/386,217
PRIORITY FILING DATE: 2002-09-19
PRIORITY APPLICATION NUMBER: US 60/386,218
PRIORITY FILING DATE: 2002-09-19
PRIORITY APPLICATION NUMBER: US 60/386,219

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PRIOR FILING DATE: 2002-09-19
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 19
 LENGTH: 1494
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: N. Aestuarii-like AOB P4clone31 16S rDNA
 US-10-659-948A-19

Query Match 93.3%; Score 1359.2; DB 7; Length 1494;
 Best Local Similarity 96.3%; Pred. No. 0;
 Matches 1402; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

1 ATTGAACGCTGGCGGAGTCTTATACATGCAAGTCGACGCGACGAGTCTTGACAT 60
 19 ATTGAACGCTGGCGGAGTCTTATACATGCAAGTCGACGCGACGAGTCTTGACAT 78
 61 CTGGTGGCGAGTGGCGGACGGGTGATGATGCAATCGGAACGTATCCAGAAAGAGGGGGA 120
 79 CTGGTGGCGAGTGGCGGACGGGTGATGATGCAATCGGAACGTATCCAGAAAGTGGGGAT 138
 121 ACGCATCGAAAGATGTCTAATACCGCATATCTTAAGGAGGAAAGCGGAGTGA 180
 139 ACGCATCGAAAGATGTCTAATACCGCATATCTTAAGGAGGAAAGCGGAGTGA 198
 181 GACCTTGGCTTTGGAGCGCGGATGTCTGATTAGTGTGGGGTAAAGGCTTAC 240
 199 GACCTTGGCTTTGGAGCGCGGATGTCTGATTAGTGTGGGGTAAAGGCTTAC 258
 241 CAAGGCGAGTCAATGATGTTGTTCTGAGAGAGACGACGCAACCTTGGGCTTAC 300
 259 CAAGGCGAGTCAATGATGTTGTTCTGAGAGAGACGACGCAACCTTGGGCTTAC 318
 301 GCCCAGACTCTTACGGGAGGACAGTGGGGAAATTTTGACAAATGGGCGCAAGCTGATC 360
 319 GCCCAGACTCTTACGGGAGGACAGTGGGGAAATTTTGACAAATGGGCGCAAGCTGATC 378
 361 CAGCAATGCGCGGTAGTGAAGAGGCTTGGGGTGTAAAGCTTTTCAGTGAAGA 420
 379 CAGCAATGCGCGGTAGTGAAGAGGCTTGGGGTGTAAAGCTTTTCAGTGAAGA 438
 421 AAAGGTAGGTAATATATGATGATCAATGATGATGATGATGATGATGATGATGATGAT 480
 439 AAAGGTAGGTAATATATGATGATCAATGATGATGATGATGATGATGATGATGATGAT 498
 481 TAGGTCCAGACGCGCGGTATACGTAGGAGTCAAGCGTTAATCGGAATTAATCGGCGCT 540
 499 TAGGTCCAGACGCGCGGTATACGTAGGAGTCAAGCGTTAATCGGAATTAATCGGCGCT 558
 541 AAAGGTAGGTAATATATGATGATCAATGATGATGATGATGATGATGATGATGATGAT 600
 559 AAAGGTAGGTAATATATGATGATCAATGATGATGATGATGATGATGATGATGATGAT 618
 601 TGGTGTGAATCTCAAGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 619 TGGTGTGAATCTCAAGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
 661 TGAATAGCTAGAGATATGAGAAATCATGATGGCGAAGGACGCTCTGGGTAAACAT 720
 679 TGAATAGCTAGAGATATGAGAAATCATGATGGCGAAGGACGCTCTGGGTAAACAT 738
 721 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGATTAGATCCTGTGATGCCGCC 780
 739 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGATTAGATCCTGTGATGCCGCC 798
 781 CTAAAGAGATCAATAGTGTGGGCTTATATAGGCTGTGTAACGAAGTAAACGCGTGA 840
 799 CTAAAGAGATCAATAGTGTGGGCTTATATAGGCTGTGTAACGAAGTAAACGCGTGA 858
 841 AGTTGACCGGCTGGGAGTACGCTCCAGAAATTAATCAAGGATTAATGCGGGAGCC 900

859 AGTTGACCGGCTGGGAGTACGCTCCAGAAATTAATCAAGGATTAATGCGGGAGCC 918
 901 GCAACAGCGGTGATATGATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 960
 919 GCAACAGCGGTGATATGATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 978
 961 GACATGTAGCAATTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
 979 GACATGTAGCAATTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
 1020 GCATGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1079
 1039 GCATGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1098
 1080 CTTGTCTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
 1099 CTTGTCTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1158
 1140 GGAGGAAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1199
 1159 GGAGGAAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1218
 1200 ATCAATGCGCGGTACAGAGGTTGCCAACCCGAGAGGAGTAAATCTCAGAAAGCGC 1259
 1219 ATCAATGCGCGGTACAGAGGTTGCCAACCCGAGAGGAGTAAATCTCAGAAAGCGC 1278
 1260 GTGTGATGCTCGGATGAGGATCTGCACTGCACTCGGTAAGTGGATGCTGATGATGATGATGAT 1319
 1279 GTGTGATGCTCGGATGAGGATCTGCACTGCACTCGGTAAGTGGATGCTGATGATGATGATGAT 1338
 1320 CGGATCAGCATGCTCGGATGAGGATCTGCACTGCACTCGGTAAGTGGATGCTGATGATGATGATGAT 1379
 1339 CGGATCAGCATGCTCGGATGAGGATCTGCACTGCACTCGGTAAGTGGATGCTGATGATGATGATGAT 1398
 1380 TGGAGTGGGTTTCAACGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1439
 1399 TGGAGTGGGTTTCAACGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1458
 1440 AATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1455
 1459 TGGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1474

RESULT 11
 US-10-659-980A-19
 : Publication 19, Application US/10659980A
 : Sequence 19, US20040106133A1
 : GENERAL INFORMATION:
 : APPLICANT: Hovaneq, Timothy A
 : TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
 : FILE REFERENCE: 81289-284781
 : CURRENT APPLICATION NUMBER: US/10/659,980A
 : PRIOR FILING DATE: 2003-09-10
 : PRIOR APPLICATION NUMBER: US 09/573,684
 : PRIOR FILING DATE: 2000-05-19
 : PRIOR APPLICATION NUMBER: US 60/386,217
 : PRIOR FILING DATE: 2002-09-19
 : PRIOR APPLICATION NUMBER: US 60/386,218
 : PRIOR FILING DATE: 2002-09-19
 : PRIOR APPLICATION NUMBER: US 60/386,219
 : PRIOR FILING DATE: 2002-09-19
 : NUMBER OF SEQ ID NOS: 23
 : SOFTWARE: PatentIn version 3.2
 : SEQ ID NO 19
 : LENGTH: 1494
 : TYPE: DNA
 : ORGANISM: Unknown
 : FEATURE:
 : OTHER INFORMATION: N. Aestuarii-like AOB P4clone31 16S rDNA
 US-10-659-980A-19

Query Match 93.3%; Score 1359.2; DB 7; Length 1494;
 Best Local Similarity 96.3%; Pred. No. 0;


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QY 181 GACCTTGCCTTTTGGAGCGGCGCATGTCTGATTAGCTAGTGGTGGGTTAAAGCCTTAC 240
DB 199 GACCTTGTGTCTTTTGGAGCGGCGCATGCTGATTAGCTAGTGGTGGGTTAAAGCCTTAC 258
QY 241 CAAGGCGACGATCAGTAGTGGTCTGAGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300
DB 259 CAAGGCGACGATCAGTAGTGGTCTGAGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 318
QY 301 GCCCAGACTCTTACGAGGAGGAGCAGTGGGGAATTTTGAAGATGGGCGCAAGCCTGATC 360
DB 319 GCCCAGACTCTTACGAGGAGGAGCAGTGGGGAATTTTGAAGATGGGCGCAAGCCTGATC 378
QY 361 CAGCAATGCCCGCTGAGTGAAGAGGCTTGGGTTGAAGCTCTTCACTGAGAGAGA 420
DB 379 CAGCAATGCCCGCTGAGTGAAGAGGCTTGGGTTGAAGCTCTTCACTGAGAGAGA 438
QY 421 AAAGTTACGGTAATATATGCTGATCATGACGGTATCGACAGAGAGAGCAGCGGCTAAC 480
DB 439 AAAGTTGTGATCTAATATATCAAACTTATGACGGTATCGACAGAGAGAGCAGCGGCTAAC 498
QY 481 TAGCTGCAGCAGCGCGGTAATAGTAGGGTGCAGCGTTAATCGGAATTAATCTGGGCGT 540
DB 499 TAGCTGCAGCAGCGCGGTAATAGTAGGGTGCAGCGTTAATCGGAATTAATCTGGGCGT 558
QY 541 AAAGGCTGCCAGCGGCTTTGTAGTCAATGTGAATCCCGGGGCTTAACCTGGGAAT 600
DB 559 AAAGGCTGCCAGCGGCTTTGTAGTCAATGTGAATCCCGGGGCTTAACCTGGGAAT 618
QY 601 TGCGTTGAAGCTCAAGAGCTAGAGTGGGAGAGGAGTGAATCCAGTGTAGCAG 660
DB 619 TGCGTTGAAGCTCAAGAGCTAGAGTGGGAGAGGAGTGAATCCAGTGTAGCAG 678
QY 661 TGAATTCGTAAGATATGGAAGAACTGATGCGAAGGAGCGCTCTGGGTTAACACT 720
DB 679 TGAATTCGTAAGATATGGAAGAACTGATGCGAAGGAGCGCGCTCTGGGTTAACACT 738
QY 721 GAGGCTCATGACGAAAGCGTGGGAGAGCAAGAGTTAGTACCTGATGTCAGAGCC 780
DB 739 GAGGCTCATGACGAAAGCGTGGGAGAGCAAGAGTTAGTACCTGATGTCAGAGCC 798
QY 781 CTAACGATGTCACTAGTGTGGGCTTATTAGGCTGTGTAAGAGCTAACGCGTGA 840
DB 799 CTAACGATGTCACTAGTGTGGGCTTATTAGGCTGTGTAAGAGCTAACGCGTGA 858
QY 841 AGTTGACCGCTGGGAGTACGCTGCGAAGTTAACTCAAGAAATTGAAGGAGAGCC 900
DB 859 AGTTGACCGCTGGGAGTACGCTGCGAAGTTAACTCAAGAAATTGAAGGAGAGCC 918
QY 901 GCAAGAGCGGTGATTTATGAGATTAAATGCAACGCAAAACCTTAACCTAACCTT 960
DB 919 GCAAGAGCGGTGATTTATGAGATTAAATGCAACGCAAAACCTTAACCTAACCTT 978
QY 961 GACATGAGGAAATTTCTAGAGATAGATTAGT-CTTCGGGAAAGCTAACACAGTGTCT 1019
DB 979 GACATGAGGAAATTTCTAGAGATAGATTAGT-CTTCGGGAAAGCTAACACAGTGTCT 1038
QY 1020 GCATGCGTGTCTGAGCTGCTGTGAGATGTTGGGTTAAGTCCGCAACGAGCGCAAC 1079
DB 1039 GCATGCGTGTCTGAGCTGCTGTGAGATGTTGGGTTAAGTCCGCAACGAGCGCAAC 1098
QY 1080 CATTGTCAATTAATGTCATATTTGTTGGGCACTTTAAAGAGATGCGGTTGCAAGC 1139
DB 1099 CATTGTCAATTAATGTCATATTTGTTGGGCACTTTAAAGAGATGCGGTTGCAAGC 1158
QY 1140 GAGAGAGTGGGAGTGAAGTCAAGTCTCATGCGCTTATGAGTGGGCTTTCACAGTGA 1199
DB 1159 GAGAGAGTGGGAGTGAAGTCAAGTCTCATGCGCTTATGAGTGGGCTTTCACAGTGA 1218
QY 1200 ATACAAATGGGCGTGAAGAGGTTGCAACCGGAGGAGGAGGTAATTCAGAAAGCC 1259
DB 1219 ATACAAATGGGCGTGAAGAGGTTGCAACCGGAGGAGGAGGTAATTCAGAAAGCC 1278

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QY 1260 GTGTAGTCCGATCCGAGTCTGCAACTGCACTCCGNGAAGTGGAGTCTAGTAATCG 1319
DB 1279 GTGTAGTCCGATCCGAGTCTGCAACTGCACTCCGNGAAGTGGAGTCTAGTAATCG 1338
QY 1320 CGGATCAGCATGTGCGGCTGATATACGTTCCCGGGTCTTTGACACCGCGCTGACCA 1379
DB 1339 CGGATCAGCATGTGCGGCTGATATACGTTCCCGGGTCTTTGACACCGCGCTGACCA 1398
QY 1380 TGGAGTGGGTTTACCAAGAGAGTGTCTTAACCTGTAAGAGGCGCTTGGCAGGTTG 1439
DB 1399 TGGAGTGGGTTTACCAAGAGAGTGTCTTAACCTGTAAGAGGCGCTTGGCAGGTTG 1458
QY 1440 AGATCATGACTGGGG 1455
DB 1459 TGCTCAATGACTTGGG 1474

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RESULT 13

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US-10-659-948a-18
; Sequence 18, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovane, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent version 3.2
; SEQ ID NO 18
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB Pacloned42-16S rDNA
US-10-659-948a-18

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Query Match 93.3%; Score 1358.8; DB 7; Length 1467;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

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QY 1 ATTGAACGCTGGGCGGATGCTTTACATGCAAGTGCAGCGGAGCAGGATGCTTGCAT 60
DB 16 ATTGAACGCTGGGCGGATGCTTTACATGCAAGTGCAGCGGAGCAGGATGCTTGCAT 75
QY 61 CTGTGGCGAGTGGCGGAGCGGTGAGTAAATGCAATCGGAAGTATCCAGAGAGCGGGGTA 120
DB 76 CTGTGGCGAGTGGCGGAGCGGTGAGTAAATGCAATCGGAAGTATCCAGAGAGCGGGGTA 135
QY 121 ACCGATCGAAAGATGTGCTAATACCGCATATATCTTAAGAGAGAAAGCAGGGATGAAA 180
DB 136 ACCGATCGAAAGATGTGCTAATACCGCATATATCTTAAGAGAGAAAGCAGGGATGAAA 195
QY 181 GACCTTGCCTTTTGGAGGGGCGGATGCTGATTAGCTAGTGGTGGGTTAAAGGCTTAC 240
DB 196 GACCTTGTGTTTGGAGGGGCGGATGCTGATTAGCTAGTGGTGGGTTAAAGGCTTAC 255
QY 241 CAAGGCGACGATCAGTAGTGGTCTGAGAGAGCAGACAGCAGCAGCAGTGGAGCTGAGACAG 300
DB 256 CAAGGCGACGATCAGTAGTGGTCTGAGAGAGCAGACAGCAGCAGCAGTGGAGCTGAGACAG 315
QY 301 GCCCAAGCTCTTACGAGGAGCAGCAGTGGGAAATTTTGAACAATGGGCGCAAGCTGATC 360
DB 316 GCCCAAGCTCTTACGAGGAGCAGCAGTGGGAAATTTTGAACAATGGGCGCAAGCTGATC 375

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Db      555 AAAGGGGCGAGCGGCTTTGTAAGTCAGATGTAATCCCGGCTTAACTGGGAT 614
Qy      601 TGCCTTTGAAACTCAAGAGCTAGAGTGTGCGAGGAGGTGAATTCATGTGTACAG 660
Db      615 TCGCTTTGAAACTCAAGAGCTAGAGTGTGCGAGGAGGTGAATTCATGTGTACAG 674
Qy      661 TGAATTCGTAGAGATATGGAAGAACATCGATGCGGAAGGACGCTCTGGGTTAACT 720
Db      675 TGAATTCGTAGAGATATGGAAGAACATCGATGCGGAAGGACGCTCTGGGTTAACT 734
Qy      721 GAGGCTATGACGAAGGCGGGGAGGAACAGAGATTAGATCCCTGTGTACAGGCC 780
Db      735 GAGGCTATGACGAAGGCGGGGAGGAACAGAGATTAGATCCCTGTGTACAGGCC 794
Qy      781 CTAACGATGTCAACTAGTGTGTGGGCTTTATAGGCTGTGTAAAGAGCTAACGCGTGA 840
Db      795 CTAACGATGTCAACTAGTGTGTGGGCTTTATAGGCTGTGTAAAGAGCTAACGCGTGA 854
Qy      841 AGTTGACCGGCTGGGAGTACGCTGCGCAAGTTAAACTCAAGAGATTGACGGGAGCCC 900
Db      855 AGTTGACCGGCTGGGAGTACGCTGCGCAAGTTAAACTCAAGAGATTGACGGGAGCCC 914
Qy      901 GCAACAGCGGTGATTAATGATTAATTCGATGCAACGCGAAACCTTACCTACCTT 960
Db      915 GCACAAACGCTGATTAATGATTAATTCGATGCAACGCGAAACCTTACCTACCTT 974
Qy      961 GACATGAGCAATTTTCTAGAGATAGATTAGTGC-TTCGGGAAACGCTAACACAGGTCT 1019
Db      975 GACATGAGCAATTTTCTAGAGATAGATTAGTGC-TTCGGGAAACGCTAACACAGGTCT 1034
Qy      1020 GCATGCGCTGTCTCACTCTGTGTGTGAGATGTTGGGTTAACTCCCGCAACGACCGCAC 1079
Db      1035 GCATGCGCTGTCTCACTCTGTGTGTGAGATGTTGGGTTAACTCCCGCAACGACCGCAC 1094
Qy      1080 CTTGTCAATTAATGGCCATCATTTGTTGGGACCTTTAATGAGCTGCGGTTGACAAACC 1139
Db      1095 CTTGTCAATTAATGGCCATCATTTGTTGGGACCTTTAATGAGCTGCGGTTGACAAACC 1154
Qy      1140 GAGAGAGGTGGGAGTACAGTCAAGTCTCTCACTGCGCTTATGGGTAGGGCTTCAACGTA 1199
Db      1155 GAGAGAGGTGGGAGTACAGTCAAGTCTCTCACTGCGCTTATGGGTAGGGCTTCAACGTA 1214
Qy      1200 ATACAAATGGGCGCTACAGAGGTTGCCAACCCCGAGGGGAGGCTAATCTAGAAAGGCC 1259
Db      1215 ATACAAATGGGCGCTACAGAGGTTGCCAACCCCGAGGGGAGGCTAATCTAGAAAGGCC 1274
Qy      1260 GTGCTAGTCCGGATCGGAGTGTGCAACTGCACTCGTGAAGTCGGAATCGCTAGTAATCG 1319
Db      1275 GTGCTAGTCCGGATCGGAGTGTGCAACTGCACTCGTGAAGTCGGAATCGCTAGTAATCG 1334
Qy      1320 CGGATCAGCATGTGCGCGGTGAATCGTTCCCGGGTCTTGTATCACACCGCCCGTCAACA 1379
Db      1335 CGGATCAGCATGTGCGCGGTGAATCGTTCCCGGGTCTTGTATCACACCGCCCGTCAACA 1394
Qy      1380 TGGGAGTGGGTTTACAGAGAGCGTGTAAACCTTAAGAGAGGGGCTTGGCCAGCGTG 1439
Db      1395 TGGGAGTGGGTTTACAGAGAGCGTGTAAACCTTAAGAGAGGGGCTTGGCCAGCGTG 1453
Qy      1440 AGATTCACTGACTGG 1453
Db      1454 AGATTCACTGACTGG 1467

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RESULT 15
US-10-659-983A-18
; Sequence 18, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A

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CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent version 3.2
; SEQ ID NO 18
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB Paclone42 16S rDNA
US-10-659-983A-18

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Query Match 93.3%; Score 1358.8; DB 7; Length 1467;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

Qy      1  ATTGAAGCTGGGCGATGCTTACATGATGCAAGTGAACGCGACGCGATGCTTGCAT 60
Db      16  ATTGAAGCTGGGCGATGCTTACATGATGCAAGTGAACGCGACGCGATGCTTGCAT 75
Qy      61  CTGTGGCGAGTGGCGGACCGGTGAGTAATGATCGGAACGTAATCCAGAAAGGGGGTA 120
Db      76  CTGTGGCGAGTGGCGGACCGGTGAGTAATGATCGGAACGTAATCCAGAAAGGGGGTA 135
Qy      121  ACCGATCGAAAGATGTCATTAATCCGATATATCTTAAGGAGGAAGGAGGGATGAAA 180
Db      136  ACCGATCGAAAGATGTCATTAATCCGATATATCTTAAGGAGGAAGGAGGGATGAAA 195
Qy      181  GACCTTGCGCTTTGGAGCGGCCGATGTCTGATTAAGTATGTTGGTGGGTTAAAGCCTAC 240
Db      196  GACCTTGCGCTTTGGAGCGGCCGATGTCTGATTAAGTATGTTGGTGGGTTAAAGCCTAC 255
Qy      241  CAAGGCGACGATCAGTATGTTGTTCTGAGAGAGACGACCAACGACACTGGGACTGAGACG 300
Db      256  CAAGGCGACGATCAGTATGTTGTTCTGAGAGAGACGACCAACGACACTGGGACTGAGACG 315
Qy      301  GCCCAAGCTCTTACGGGAGGACGACGATGGGAAATTTTGAACAATGGGCCAGACCTGATC 360
Db      316  GCCCAAGCTCTTACGGGAGGACGACGATGGGAAATTTTGAACAATGGGCCAGACCTGATC 375
Qy      361  CAGCAATGCCGCGTGTGAGTAAGAGGCTTGGGTTGTAAGTCTTTCACTGAGTGAAGA 420
Db      376  CAGCAATGCCGCGTGTGAGTAAGAGGCTTGGGTTGTAAGTCTTTCACTGAGTGAAGA 434
Qy      421  AAGGTTACGGTAATTAATCTGTGATCATGACGTAATGACAGAGAGAGACGCGGCTAAC 480
Db      435  AAGGTTACGGTAATTAATCAACAATTATGATGTAACGACAGAGAGAGACGCGGCTAAC 494
Qy      481  TAGTTCACAGACCGCGGTAATACGTAGAGGTCGCAACGTTAATCCGAAATTAATGAGGCGT 540
Db      495  TAGTTCACAGACCGCGGTAATACGTAGAGGTCGCAACGTTAATCCGAAATTAATGAGGCGT 554
Qy      541  AAGGTTGCGCAGGCGGCTTTGTAAGTCAAGATGTGAATCCCGGCGCTTAACCTGGGAAT 600
Db      555  AAGGTTGCGCAGGCGGCTTTGTAAGTCAAGATGTGAATCCCGGCGCTTAACCTGGGAAT 614
Qy      601  TGCCTTTGAAACTCAAGAGCTAGAGTGTGCGAGGAGGTGAATTCATGTGTACAG 660
Db      615  TGCCTTTGAAACTCAAGAGCTAGAGTGTGCGAGGAGGTGAATTCATGTGTACAG 674
Qy      661  TGAATTCGTAGAGATATGGAAGAACATCGATGCGGAAGGACGCTCTGGGTTAACT 720
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Qy      721  GAGGCTATGACGAAGGCGGGGAGGAACAGAGATTAGATCCCTGTGTACAGGCC 780
Db      735  GAGGCTATGACGAAGGCGGGGAGGAACAGAGATTAGATCCCTGTGTACAGGCC 794

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Db 735 GACGCTCATGACGAAAGCGTGGGGAGCAAAACAGATTAGATACCTGTAGTCCACGCC 794
QY 781 CTAACGATGCTCACTAGTGTGGGCTTATTAGCTTGGTAAGCAAGCTAACCGCTGA 840
Db 795 CTAACGATGCTCACTAGTGTGGGCTTACTAGGCTTGGTAAGCTAACCGCTGA 854
QY 841 AGTTGACCGCTGGGGAGTACGTCGCAAGATTAAACTCAAGGAATTGACGGGGACCC 900
Db 855 AGTTGACCGCTGGGGAGTACGTCGCAAGATTAAACTCAAGGAATTGACGGGGACCC 914
QY 901 GCACAGCGGTGATTAATGATTAATTCGATGCAAGCGGAAAACTTACTTACCCTT 960
Db 915 GCACAGCGGTGATTAATGATTAATTCGATGCAAGCGGAAAACTTACTTACCCTT 974
QY 961 GACATGTAGCCGAATTTCTAAGATAGATTAGTC-TTCGGGAACCTTAACAGAGTGT 1019
Db 975 GACATGTAGCCGAATTTCTAAGATAGATTAGTC-TTCGGGAACCTTAACAGAGTGT 1034
QY 1020 GCATGCTGTGCTGACGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079
Db 1035 GCATGCTGTGCTGACGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
QY 1080 CTTTGTCAATTAATTCGATCAATTTGGTGGGCACTTTAATGAGACTGCCGGTGACAAAC 1139
Db 1095 CTTTGTCAATTAATTCGATCAATTTGGTGGGCACTTTAATGAGACTGCCGGTGACAAAC 1154
QY 1140 GGAGGAAGGTGGGGATGACGTCGAAGTCTCATGGCCCTTATGGGTAGGGCTTCAACGTA 1199
Db 1155 GGAGGAAGGTGGGGATGACGTCGAAGTCTCATGGCCCTTATGGGTAGGGCTTCAACGTA 1214
QY 1200 ATACAAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1259
Db 1215 ATACAAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1274
QY 1260 GTGCTAGTCCGATCGAGTCTGCAACTGCACTCCGTGAAGTCGATAGTAATCG 1319
Db 1275 GTGCTAGTCCGATCGAGTCTGCAACTGCACTCCGTGAAGTCGATAGTAATCG 1334
QY 1320 CGGATCAGCATGTGGCGGTGAATAGTTCGCGGGTCTTGTACACACCGCCGTCACACCA 1379
Db 1335 CGGATCAGCATGTGGCGGTGAATAGTTCGCGGGTCTTGTACACACCGCCGTCACACCA 1394
QY 1380 TGGGAGTGGGTTTCCACGAGACAGTAGTCTAACCGTAAGGAGGGCGCTGGCCAGGCTG 1439
Db 1395 TGGGAGTGGGTTTCCACGAGACAGTAGTCTAACCGTAAGGAGGGCGCTGGCCAGGCTG 1453
QY 1440 AGATTCAATGACTGG 1453
Db 1454 AGATTCAATGACTGG 1467

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Search completed: April 6, 2006, 23:35:31
 Job time : 1288 secs

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Qy	177	GAAGAAGCTTGGGCTTTTGGAGAGGGCCCATGCTGATTAATAGCTAATTTGGTGGGGTTAAAGCC	236
Db	209	TTCCGGGCTTGGGCTATCCGAAGCGGCCGATATCTGAATTAAGCTGGTGGGGGGTTAAAGGC	268
Qy	237	CTACCAAGGCGCAGATCAGTACGATTAATTTGGTCTGAGAGACGACACGACACTGGGAGCTGAGA	296
Db	269	CCACCAAGGCGCAGATCAGTACGATTAATTTGGTCTGAGAGAGTATCCGCCACACTGGGAGCTGAGA	328
Qy	297	CACGGCCCAAGACTCTTAAGGAGAGGACGAGTGGGGAAATTTTGGACATATGGCGCAAGCTT	356
Db	329	CACGGCCCAAGACTCTTAAGGAGAGGACGAGTGGGGAAATTTTGGACATATGGGGCAAGCTT	388
Qy	357	GATCAGCAATGCGCGGTGAGAGGAAGAGGCTTGGGGTTGTAAGTCTTTCAATCGAGC	416
Db	389	GATCAGCAATGCGCGGTGAGAGGAAGAGGCTTGGGGTTGTAAGTCTTTCAATCGAGG	448
Qy	417	AAGAAAGGTTACGGTAATAATATCTGATCTCAATGACCGATATGACAGAGAAAGACCGGC	476
Db	449	AAGAAAGGCTGTTGTCCTCAATATCGGCGCGGCGCAATGACCGTATCTGAAGAAATAGACACCGGC	508
Qy	477	TAACTACGTCGACAGAGCCGCGGTAAATCTTACGATGGTGAACAGGCTTAATCCGAAATTAATGCG	536
Db	509	TAACTACGTCGACAGAGCCGCGGTAAATCTTACGATGGTGAACAGGCTTAATCCGAAATTAATGCG	568
Qy	537	GCGTAAAGGGTGCAGAGCGGCTTTGTAACTGATGATGTAATCCCGGGCTTAACTGCG	596
Db	569	GCGTAAAGCGGCGCGAGACGGTTACTTTAAGCAGAGATGTGAATCCCGGGCGTCAACCGCG	628
Qy	597	GAATTCGCTTTGAATACTACAGGCTTAGAGTGTGGCAGAGGAGGTGGAATTCATGCTGA	656
Db	629	GAATTCGCTTTGMACTGAGTGAATCTGAGTGTGACAGGGAGGTGGAATTCAGTGTGA	688
Qy	657	GCACTGAAGTGGGTGAGATATGGAAGAAATCATGATGGCGAAGGACGCTCTCGGTGTTAA	716
Db	689	GCACTGAAGTGGGTGAGATATGGAAGAAATCATGATGGCGAAGGACGCTCTCGGTGATTA	748
Qy	717	CACCTGACGCTCAATGACGAAAGCGTGGGAGGCAAAACAGATTAAGTACCTCGTGTGCTCA	776
Db	749	CACCTGACGCTCAATGCTCCGAAACGTTGGGTGCAAAACAGATTAAGTACCTCGTGTGCTCA	808
Qy	777	CGCCCTTAACCATGTCATCTAATTTTGGGCGCTTTTA- GCGTTGGTAAACGAAGCTAACG	835
Db	809	CGCCCTTAACCATGTCATCTAATTTTGGGCGCTTTTAATGCTTGTGTAGCGTAAAGCTAACG	868
Qy	836	CGTGAAGTTGACCGGCTGGGAGTATCGGTGCGAAGATTAAACTCAAGAAATTAAGACGGG	895
Db	869	CGTGAAGTTGACCGGCTGGGAGTATCGGTGCGAAGATTAAACTCAAGAAATTAAGACGGG	928
Qy	896	GAACCCGCAACAGCGGTGATTAATGTGATTAATTTGATGCAACGGGAAAACTTAACTTA	955
Db	929	GAACCCGCAACAGCGGTGATTAATGTGATTAATTTGATGCAACGGGAAAACTTAACTTA	988
Qy	956	CCCTTGAATGATGAGGAATTTTCTTGAAGATAGATTAGTG- CTTGCGGAAACGCTAACACAG	1014
Db	989	GTTTGTGAATGTGCGGAATCTCTCCGGAACGAGAGAGTGTCTCTCGGAGCCGTAACACAG	1048
Qy	1015	GTGCTGACATGCGTGTGTCAGCTCGTGTGTGTGAGATGTTGGTTAATGTCCTCGGACAGAGC	1074
Db	1049	GTGCTGACATGCGTGTGTCAGCTCGTGTGTGTGAGATGTTGGTTAATGTCCTCGGACAGAGC	1108
Qy	1075	GCAACCCCTTGTCAATTAATTTGCAATTAATTTGGTGGGCACTTAAAGACATGCGCGGTAC	1133
Db	1109	GCAACCCCTTGTCAATTAATTTGCAATTAATTTGGTGGGCACTTAAAGACATGCGCGGTAC	1166
Qy	1135	AAACCCGAGAAAGTGGGAGTACGTCATGATCTCATGGCCCTTATGGGTTGGGCTTCAAC	1194
Db	1169	AAACCCGAGAAAGTGGGAGTACGTCATGATCTCATGGCCCTTATGGGTTGGGCTTCAAC	1222
Qy	1195	ACGTTAATCAATGGCGGTATACAGAGGTTGCCAACCCGAGAGGGAGGAGCTAATCTACAA	1254
Db	1229	ACGTTAATCAATGGCGGTATACAGAGGTTGCCAACCCGAGAGGGAGGAGCTAATCTACAA	1288

OY	1255	AGCGGCTGTACGTCCGGATCGSAGTCTGCAACTCGATTCCGTGAAGTCGGAATGCTTAGT	13174
Db	1289	AACCGATGTAGTCCGATTGCATCTTGCACTTCGATCATGAATGTCGAAATGCTTAGT	1348
OY	1315	AATCGCGATTCAGCATGTCCGCGTGAATACTTCCGGGTCTTTGTACACAACCGCCGCTCA	1374
Db	1349	AATCGCAGGTTCAGCATACTCGGATGAAATACGTTCCGGGTCTTTGTACACAACCGCCGCTCA	1408
OY	1375	CACCATGGAAGTGGGTTTACACAGAAGCAGTAAGTCTAACCGTAAAGAGGGCGTTGCCA	1434
Db	1409	CACCATGGGAGTGGGGGATACCGAAGATAGTAGGGTAACCGCAAGAGTCCGCTTACCA	1468
OY	1435	CGGTAGATTCATGACTGGGGGT	1457
Db	1469	CGGTATGCTTCATGACTGGGGGT	1491
RESULT 3			
US-08-114-695A-7			
Sequence 7, Application US/08114695A			
Patent No. 5508193			
GENERAL INFORMATION:			
APPLICANT: Mandelbaum, Raphael T.			
APPLICANT: Macetle, Lawrence P.			
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND			
TITLE OF INVENTION: WATER			
NUMBER OF SEQUENCES: 8			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.			
STREET: 3500 IDS CENTER			
CITY: MINNEAPOLIS			
STATE: MN			
COUNTRY: USA			
ZIP: 55402			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentln Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/114,695A			
FILING DATE: 31-AUG-1993			
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
NAME: MUEITING, ANN M.			
REGISTRATION NUMBER: 33,977			
REFERENCE/DOCKET NUMBER: 600.268US1			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 612-339-0331			
TELEFAX: 612-339-3061			
INFORMATION FOR SEQ ID NO: 7:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1536 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: rRNA			
ORIGINAL SOURCE:			
ORGANISM: Pseudomonas testosteroni			
US-08-114-695A-7			
Query Match 76.7%; Score 118.2; DB 2; Length 1536;			
Best Local Similarity 70.0%; Pred. No. 0;			
Matches 1022; Conservative 25%; Mismatches 178; Indels 9; Gaps 4;			
OY	1	ATTGAACGCTGCGGCAT-GCTTTACATGCAAGTCTGAACGGCACACGATCGATGCTTGA	59
Db	28	AUTGAAGCGCGGGCGGCAKUNGCUCUUAACAUGCAGGCGAAGCGUAAACAGUCUCUCG--	84
OY	60	TCTGGTGGCAGTGGGGGACGGGTGATGATGCATGGAACGTAACAGAGAGGGGGGT	119
Db	85	-AUGCUACAAGUGGCGAAGCGGUGAUUACUACGGAACGUGCCUAGUAGGGGGAU	143

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QY 120 AAGCATCGAAGATGCTAATACCGCATATCTTAAGAGAGAAAGAGGAGATCGAA 179
DB 144 AACUACUCGAAAGAGUAGCUAUAUCCGCAUGAUAUACGAAUGAAAGCAGGGGACUUC 203
QY 180 AGACCTTGCCCTTTTGAAGGGCCGATGCTGATTAAGTAAAGGCTTAAGGCTTA 239
DB 204 GGGCCUUGUCUUAAGAGGGCGUAGAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 263
QY 240 CCAAGGCGAAGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 299
DB 264 CCAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323
QY 300 GGGCCGATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
DB 324 GGGCCGATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
QY 360 CCAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
DB 384 CCAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 443
QY 420 AAGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
DB 444 AAGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503
QY 480 CTAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
DB 504 CTAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 563
QY 540 TAAAGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599
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DB 924 CCAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 983
QY 960 TGAAGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1016
DB 984 TGAAGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1043
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DB 1163 ACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1222

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QY 1257 CGCGTGTAGTCGCGATCGGATGCTGCAACTGCACTCCGTAAGTGGAAATGCTAGTAA 1316
DB 1283 CCAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342
QY 1317 TCGCGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1376
DB 1343 TCGCGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1402
QY 1377 CCAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1436
DB 1403 CCAAGGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1462
QY 1437 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1483
DB 1463 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

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; Sequence 1, Application US/09342579
; Patent No. 6187569
; GENERAL INFORMATION:
; APPLICANT: BRAMUCCI, MICHAEL G.
; APPLICANT: MCCURTEN, CAROL M.
; APPLICANT: NAGARAJAN, VASANTHA
; APPLICANT: THOMAS, STUART M.
; TITLE OF INVENTION: Microbial Production of Terephthalic Acid and
; FILE REFERENCE: CL-1257
; CURRENT APPLICATION NUMBER: US/09/342,579
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/091,645
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Burkholderia sp.
US-09-342-579-1

Query Match 76.0%; Score 1108; DB 3; Length 1451;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1252; Conservative 0; Mismatches 175; Indels 9; Gaps 3;

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Qy 371 GCGTGAAGTGAAGAGCCCTCGGCTTGAAGCTCTTTCAGTCGAGAGAAAGGTTACG 430
Db 371 GCGTGTGTAAGAAAGCCCTTCGGCTTGTAAAGCATTCTTCCGGAAGAAATCTCTCG 430
Qy 431 GTAAATAATCGTACTCATGACGATGACAGAAAGACACCGCTTAATCTACGTCGAG 490
Db 431 GTTAATACTCGGGGGGATGACGATGACGGAATAAGCACCGCTTAATCTACTTGCA 489
Qy 491 CAGCCGCGTAAATAGTAGGGGTCAGAGGCTTAATCGGAAATTAATCGGGGTTAAAGGTCG 550
Db 490 CAGCCGCGTAAATAGTAGGGGTCAGAGGCTTAATCGGAAATTAATCGGGGTTAAAGGTCG 549
Qy 551 CAGCGCGCTTTGTAAGTCAAGATGTAATAATCCCGGGCTTAATCGTGAATTCGTTTAA 610
Db 550 CAGCGCGCTTTGTAAGTCAAGATGTAATAATCCCGGGCTTAATCGTGAATTCGTTTAA 609
Qy 611 ACTCAAGGCTTAAGATGTGGCAGAGGAGGTAATTCATGTGTAGCAAGTAAATGCGT 670
Db 610 ACTGCAAGGCTTAAGATGTGGCAGAGGAGGTAATTCATGTGTAGCAAGTAAATGCGT 669
Qy 671 AGAGATATGAGAAAGACATGATGCGAAGGCGAGCTCTCGGTGTAACATGACGTCATG 730
Db 670 AGAGATATGAGAAAGACATGATGCGAAGGCGAGCTCTCGGTGTAACATGACGTCATG 729
Qy 731 CACGAAAGCGTGGGAGCAACAGATTAAGTACCTCGTGTAGTCCACGCGCTTAACGATG 790
Db 730 CACGAAAGCGTGGGAGCAACAGATTAAGTACCTCGTGTAGTCCACGCGCTTAACGATG 789
Qy 791 TCAACTAGTGTGGGCTTATTTAGGCTTGTGAAGAACTTAACGCTGAAGTTGACCGC 850
Db 790 TCAACTAGTGTGGGCTTATTTAGGCTTGTGAAGAACTTAACGCTGAAGTTGACCGC 849
Qy 851 CTGGGAGTACGTCGTGCAAGATTAATCAAGAAATTAACGGGAGACCGGCAAGGCG 910
Db 850 CTGGGAGTACGTCGTGCAAGATTAATCAAGAAATTAACGGGAGACCGGCAAGGCG 909
Qy 911 TGAATTAATGTGAATTAATTCATGACAGCGAAACCTTACCTTGCATGTAGC 970
Db 910 TGAATTAATGTGAATTAATTCATGACAGCGAAACCTTACCTTGCATGTAGC 969
Qy 971 GAAATTTCTAGAGATAGATTAAGTCTCTCTGGAAAGCTTAACAGAGTGTGATGCT 1027
Db 970 GAAATTTCTAGAGATAGATTAAGTCTCTCTGGAAAGCTTAACAGAGTGTGATGCT 1029
Qy 1028 GTGCTGACGCTGTGTCGTGAAGTGTGGGTTAATTCGCGCAACAGCGCAACCTTGTCA 1087
Db 1030 GTGCTGACGCTGTGTCGTGAAGTGTGGGTTAATTCGCGCAACAGCGCAACCTTGTCC 1089
Qy 1088 TTAATTTGCATCTTGTGGGCACTTAATGACATGCGGATGACAAACCGAGGAG 1147
Db 1090 TTAATTTGC-----TAGCGAAGCACTTAAGGAACTGCGGATGACAAACCGAGGAG 1144
Qy 1148 GTGGGATGACGTCAAGTCTCATATGCTTAATGGGTTAGGGCTTCAACGTAATCAATG 1207
Db 1145 GTGGGATGACGTCAAGTCTCATATGCTTAATGGGTTAGGGCTTCAACGTAATCAATG 1204
Qy 1208 GCGGATTAAGAGGCTTGGCAACCGCGAGGGGAGCTTAATCTCAAGAAAGCGGCTGTAGT 1267
Db 1205 GTCGATTAAGAGGCTTGGCAACCGCGAGGGGAGCTTAATCTCAAGAAAGCGGCTGTAGT 1264
Qy 1268 CCGGATCGGATGTCGCACTGCACTCGTGAAGTGCAGATGCTGTAGTATGCGGATGAG 1327
Db 1265 CCGGATCGGATGTCGCACTGCACTCGTGAAGTGCAGATGCTGTAGTATGCGGATGAG 1324
Qy 1328 CATGTGCGGATTAATGCTTCCCGGCTTGTGAACAACCGCCCTGACACATGAGAGTG 1387
Db 1325 CATGTGCGGATTAATGCTTCCCGGCTTGTGAACAACCGCCCTGACACATGAGAGTG 1384
Qy 1388 GGTTCACCAAGAGGATGCTTAACGCTAAGAGGCGGCTTGGCAAGGAGAT 1443
Db 1385 GGTTCACCAAGAGGATGCTTAACGCTAAGAGGCGGCTTGGCAAGGAGAT 1440

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RESULT 5
US-09-617-854A-1
; Sequence 1, Application US/09617854A
; Patent No. 6461840
; GENERAL INFORMATION:
; APPLICANT: BRAMUCCI, MICHAEL G.
; APPLICANT: MCCUTCHEN, CAROL M.
; APPLICANT: NAGARAJAN, VASANTHA
; APPLICANT: THOMAS, STUART M.
; TITLE OF INVENTION: Microbial Production of Terephthalic Acid and
; TITLE OF INVENTION: Isophthalic Acid
; FILE REFERENCE: CL-1257
; CURRENT APPLICATION NUMBER: US/09/617, 854A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/091,645
; PRIOR FILING DATE: JULY 2, 1998
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Burkholderia sp.
US-09-617-854A-1

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Query Match      76.0%; Score 1108; DB 3; Length 1451;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1252; Conservative 0; Mismatches 175; Indels 9; Gaps 3;

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Qy 11 GCGCGCATGCTTTTACATGCAAGTCGAACGCGACAGCGAATGCTTGCATCTGTGCGA 70
Db 11 GCGCGCATGCTTTTACATGCAAGTCGAACGCGACAGCGAATGCTTGCATCTGTGCGA 70
Qy 71 GTGGCGGACGGGTGACGTAATGCAATCCGGAAGTATCCGAAGAGGGGGGTAAAGCATGAA 130
Db 71 GTGGCGGACGGGTGACGTAATGCAATCCGGAAGTATCTGTATGGGGGATTAATCTGGCAAA 130
Qy 131 AGATGTCTATAATCCGATATTAATCTTAAGAGAGAAAGCAGGGATCGAAAGACCTTGCGC 190
Db 131 AGCGGATTAATTAACCGATATTAATCTTAAGAGAGAAAGCAGGGATCGAAAGACCTTGCGC 190
Qy 191 TTTTGAAGCGCGCATGCTGATTTAGCTAGTGTGGGTTAAAGCTTACCAAGGCGACG 250
Db 191 TACAAAGACAGCGCATGCTCAATTAATCTTGTGGGTGTTAAAGCTTACCAAGGCGACA 250
Qy 251 ATCTGTAGTGTGTGTGAGAGACGACCGCACTGCGACTGAGACACGGCCAGACTC 310
Db 251 ATCTGTAGTGTGTGTGAGAGACGACCGCACTGCGACTGAGACACGGCCAGACTC 310
Qy 311 CTACGGGAGGACAGATGGGGAAATTTTGAACAATGGGCGCAAGCTGATCAGCAATGCC 370
Db 311 CTACGGGAGGACAGATGGGGAAATTTTGAACAATGGGCGCAAGCTGATCAGCAATGCC 370
Qy 371 GCGTGAATGAAGAAAGGCTTCGAGTTGTAAAGCTCTTTCAGTGGAGAAAGGTTAGC 430
Db 371 GCGTGTGTAAAGAAAGGCTTCGAGTTGTAAAGCTCTTTCAGTGGAGAAAGGTTAGC 430
Qy 431 GTAAATAATGTGACTATATACGCTATCGACAGAAAGACACCGGCTTAATCTACTGTGCA 490
Db 431 GTTAATAATCTCGGGGGATATACGCTATCGGAAAAATTAAGACCGGCTTAATCTACTGTGCA 489
Qy 491 CAGCGCGGTAATACGTAAGGTTCAAGCGTTAATCGGAATTAATCTGGGCGTAAAGGTTGCG 550
Db 490 CAGCGCGGTAATACGTAAGGTTCAAGCGTTAATCGGAATTAATCTGGGCGTAAAGGTTGCG 549
Qy 551 CAGCGCGCTTTGTAAGTCAAGATGTAATAATCCCGGCTTAACTTGGAATTCGTTTGA 610
Db 550 CAGCGCGCTTTGTAAGTCAAGATGTAATAATCCCGGCTTAACTTGGAATTCGTTTGA 609
Qy 611 ACTCAAGGCTTAAGATGTGGCAGAGGAGGTAATTCATGTGTAGCAAGTAAATGCGT 670
Db 610 ACTGCAAGGCTTAAGATGTGGCAGAGGAGGTAATTCATGTGTAGCAAGTAAATGCGT 669
Qy 671 AGAGATATGAGAAAGACATGATGCGAAGGCGAGCTCTCGGTGTAACATGACGTCATG 730

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Db 670 AGGATGTGAGGAAATCCATGCGAAGGACGCCCTCGGCGCAATCTGACGCTCATG 729
Qy 731 CACGAAAGCGTGGGAGCAAAACAGGATTAATACCTGTAATGTCACGCCCTAAACGATG 790
Db 730 CACGAAAGCGTGGGAGCAAAACAGGATTAATACCTGTAATGTCACGCCCTAAACGATG 789
Qy 791 TCAGATAGTTGTTGGGCTTATTAAGGCTTGAAGCTTAACGCTTAAGCTTAAGCTTAAG 850
Db 790 TCAGATAGTTGTTGGGCTTATTAAGGCTTGAAGCTTAACGCTTAAGCTTAAGCTTAAG 849
Qy 851 CTGGGAGATGAGCTGCGAAGATTAAACTCAAGAAATTAAGCGGAGCGCCGCAAGCGG 910
Db 850 CTGGGAGATGAGCTGCGAAGATTAAACTCAAGAAATTAAGCGGAGCGCCGCAAGCGG 909
Qy 911 TGAATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 970
Db 910 TGAATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 969
Qy 971 GAATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1027
Db 970 GAATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1029
Qy 1028 GTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087
Db 1030 GTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089
Qy 1088 TTAATTCATCATTTGGTGGGCACTTTAATGATGATGATGATGATGATGATGATGATG 1147
Db 1090 TTAATTCATCATTTGGTGGGCACTTTAATGATGATGATGATGATGATGATGATGATG 1144
Qy 1148 GTGGGAGATGAGCTGCAAGTCTCATGCGCTTATGAGGAGGCTTCAACGTAATTAATG 1207
Db 1145 GTGGGAGATGAGCTGCAAGTCTCATGCGCTTATGAGGAGGCTTCAACGTAATTAATG 1204
Qy 1208 GCGCGTACAGAGGAGTTCGCAACCGCGAGGAGGAGCTAATCTGAAGAGCGCTGCTGAT 1267
Db 1205 GCGCGTACAGAGGAGTTCGCAACCGCGAGGAGGAGCTAATCTGAAGAGCGCTGCTGAT 1264
Qy 1268 CCGGATCGAGTCTGCAACTGCACTCGTGAATGCGTAATGCGTAATGCGGATCAG 1327
Db 1265 CCGGATCGAGTCTGCAACTGCACTCGTGAATGCGTAATGCGTAATGCGGATCAG 1324
Qy 1328 CATGTGCGGTAATGCTTCCGCGGCTTGTGTAACAACCGCGCTGCAACATGAGGAGT 1387
Db 1325 CATGTGCGGTAATGCTTCCGCGGCTTGTGTAACAACCGCGCTGCAACATGAGGAGT 1384
Qy 1388 GGTTCACAGAGAGCTGATCTTAACCTTAAGAGAGGCGCTTGCCACGCTGAGAT 1443
Db 1385 GGTTCACAGAGAGCTGATCTTAACCTTAAGAGAGGCGCTTGCCACGCTGAGAT 1440

```

RESULT 6
US-08-642-229A-2
Sequence 2, Application US/08642229A
Patent No. 5874291

GENERAL INFORMATION:

APPLICANT: Herwig, Russell P.
APPLICANT: Bielefeldt, Angela R.
APPLICANT: Stensel, H. David
APPLICANT: Strand, Stuart E.
TITLE OF INVENTION: Degradation of Environmental Toxins by a
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: WA 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,229A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/246,865
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: UOFW19233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
DESCRIPTION: "16S ribosomal DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brachyomonas denitrificans AS-P1
US-08-642-229A-2

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Query Match 75.9%; Score 1105.6; DB 2; Length 1452;

Best Local Similarity 86.3%; Pred. No. 0; Mismatches 189; Indels 11; Gaps 3;

Matches 1260; Conservative 0;

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Qy 1 ATTGAACGCTGGCGGAGCTCTTAAACATGCAAGTGAACGCGACGAGCTTGCAT 60
Db 1 ATTGAACGCTGGCGGAGCTCTTAAACATGCAAGTGAACGCGACGAGCTTGCAT 57
Qy 61 CTGTGCGAGTGGCGGAGCGGTGAGTAATGATCGGAAAGCTATCCAGAAAGGCGGAT 120
Db 58 ATGTGACGAGTGGCGGAGCGGTGAGTAATGATCGGAAAGCTATCCAGAAAGGCGGAT 117
Qy 121 AGCATCGAAAGATGCTTAATACCGCAATATCTTAAGAGAAAGCGGGATCGAAA 180
Db 118 ACTATCGAAAGATGCTTAATACCGCAATATCTTAAGAGAAAGCGGGATCGAAA 177
Qy 181 GACCTTGCGCTTTGGAGCGCGGATGCTGATGATGATGATGATGATGATGATGATGATG 240
Db 178 GGCCTCGCGCTTACGAGCGCGGATGCTGATGATGATGATGATGATGATGATGATGATG 237
Qy 241 CAAGCGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Db 238 CAAGCGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 297
Qy 301 GCCCGACCTCTTAACGCGGAGCGGAGCGGAGGAAATTTGGAACAATGGCGCAAGCTGATC 360
Db 298 GCCCGACCTCTTAACGCGGAGCGGAGCGGAGGAAATTTGGAACAATGGCGCAAGCTGATC 357
Qy 361 CAGCATGCGCGGTGAGTAAGAAAGGCTTGGGTTGTAAGCTCTTTCAGTCTGAGAGA 420
Db 358 CAGCATGCGCGGTGAGTAAGAAAGGCTTGGGTTGTAAGCTCTTTCAGTCTGAGAGA 417
Qy 421 AAAGGTTACGTAATTAATGCTGATCAATGACGATGACGAGAAAGACCGGCTAAC 480
Db 418 AAAGGTTACGTAATTAATGCTGATCAATGACGATGACGAGAAAGACCGGCTAAC 477
Qy 481 TACGTGCGAGCGCGCGGTAATAGTAGGAGGTAAGGAGGTAATGAGAAATTAATGAGG 540
Db 478 TACGTGCGAGCGCGCGGTAATAGTAGGAGGTAAGGAGGTAATGAGAAATTAATGAGG 537
Qy 541 AAAGGTTGCGAGCGCGGCTTTGTAAGTCAATGTAATTCGCCGCGCTTAACCTGGAAT 600

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Db      673 CTAACGATGCACTGTTGTTGGAAATTCATTTTCTGATACGAAGCAACGCGTGA 614
Qy      841 AGTTGACCGCTTGGGAGTACGGTCCGAAATTTAACTCAAGGAATTGAAGGGGACCC 900
Db      613 AGTTGACCGCTTGGGAGTACGGTCCGAAATTTAACTCAAGGAATTGAAGGGGACCC 554
Qy      901 GCACAGCGGTGATTAATGATTAATTTGATGACGCAAGGAAACCTTACCTACCTT 960
Db      553 GCACAGCGGTGATTAATGATTAATTTGATGACGCAAGGAAACCTTACCTACCTT 494
Qy      961 GACATGAGCAATTTTCTAGATTAATTAAGTCT---TCGGAAACGCTAACACAGGTG 1017
Db      493 GACATGAGCAATTTTCTAGATTAATTAAGTCT---TCGGAAACGCTAACACAGGTG 434
Qy      1018 CTGCAATGCTGTGCTGACGCTGCTGCTGAGATTTGGTTAACTCCCGCAAGAGGCA 1077
Db      433 CTGCAATGCTGTGCTGACGCTGCTGCTGAGATTTGGTTAACTCCCGCAAGAGGCA 374
Qy      1078 ACCCTGTCAATTAATTCATCAATTTGTTGGGCACTTAATGAGACTGCGCGTACAA 1137
Db      373 ACCCTGTCAATTAATTCATCAATTTGTTGGGCACTTAATGAGACTGCGCGTACAA 319
Qy      1138 CCGAGAGAGAGTGGGAGTGAAGTCAAGTCTCTCAATGCGCTTAATGAGGCTTACAGC 1197
Db      318 CCGAGAGAGAGTGGGAGTGAAGTCAAGTCTCTCAATGCGCTTAATGAGGCTTACAGC 259
Qy      1198 TAATACATGCGCGCTACAGAGGTTGCCAACCCGCAAGGAGAGCTTAATCTCAGAAAC 1257
Db      258 TCATACATGCGCGCTACAGAGGTTGCCAACCCGCAAGGAGAGCTTAATCTCAGAAAC 199
Qy      1258 GCGTGTGATGCGGATGCGAGTCTGCAACTGCACTCCGTAAGTGGATTCGCTAGTAAT 1317
Db      198 GAGTGTGATGCGGATGCGAGTCTGCAACTGCACTCCGTAAGTGGATTCGCTAGTAAT 139
Qy      1318 CCGGATACAGATCTCGCGGTGAATAGTTCCGCGGCTTTGTACACACCGCGCTCAC 1377
Db      138 CCGGATACAGATCTCGCGGTGAATAGTTCCGCGGCTTTGTACACACCGCGCTCAC 79
Qy      1378 CAGGAGAGTGGTTTACACGAAGCAGATGCTTAACCTTAAGAGAGGCGCTTCCACCG 1437
Db      78 CAGGAGAGTGGTTTACACGAAGTGAATAGTTAGCCCTTAACGAAGAGGCGCTTAAC 19
Qy      1438 TGAGATTCATGATCGGCG 1455
Db      18 CAGGATTCGATGATCGGCG 1

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RESULT 8
US-08-642-229A-3
Sequence 3, Application US/08642229A
Patent No. 5874291
GENERAL INFORMATION:
APPLICANT: Herwig, Russell P.
APPLICANT: Bielefeld, Angela R.
APPLICANT: Stensel, H. David
APPLICANT: Strand, Stuart E.
TITLE OF INVENTION: Degradation of Environmental Toxins by a
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: WA 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,229A

```

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FILING DATE: 435
CLASSIFICATION: 435
PRIORITY INFORMATION: 435
APPLICATION NUMBER: US 08/246,865
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Shelness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: UOFW19233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
TELEX: 4938023
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
DESCRIPTION: "16S ribosomal DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Unknown. Possibly new species
STRAIN: A-1
US-08-642-229A-3
Query Match 75.5%, Score 1100.2, DB 2, Length 1455;
Best Local Similarity 86.8%, Pred. No. 0;
Matches 1269, Conservative 1, Mismatches 180, Indels 12, Gaps 5;
Qy      1 ATTTGAAGCTGCGCGGATGCTTTACATGATGCAAGTGAAGCGGAGAGCGGATCTGCAT 60
Db      1 ATTTGAAGCTGCGCGGATGCTTTACATGATGCAAGTGAAGCGGAGAGCGGATCTGCAT 58
Qy      61 CTGTGCGCAGTGGCGGAGCGGAGTGAATGATGATGCGAAGTATCCAGAAAGAGGAGGATTA 120
Db      59 CTGTATGCGAGTGGCGGAGCGGAGTGAATGATGATGCGAAGTATCCAGAAAGAGGAGGATTA 118
Qy      121 AGCATGGAAGATGCTTAATCCGATATATCTTAAGAGAGAAAGCAGGGGATGAAA 180
Db      119 ACTACTGGAAGATGATGATTAATCCGATGATCTACGAGATGAAAGCGGGGATGCAA 178
Qy      181 GACCTTGCGCTTTTGGAGGCGCGATGCTGATTAAGTGAATGAGGAGGATTAAGGCTTAC 240
Db      179 GACCTTGCGCTTACAGAGCGGCTGGGAGATTAAGTGAATGAGGAGGATTAAGGCTTAC 238
Qy      241 CAAAGCGAGATCAGTATGTTGCTGAGAGAGCAGACAG-CCACACTGGAATGAGAC 299
Db      239 CAAAGCGAGATCAGTATGTTGCTGAGAGAGCAGACAG-CCACACTGGAATGAGAC 298
Qy      300 GGGCCAGACTCTTACCGGAGGAGCAGAGTGGGAAATTTTGAACATGGGCGCAAGCTTAT 359
Db      299 GGGCCAGACTCTTACCGGAGGAGCAGAGTGGGAAATTTTGAACATGGGCGCAAGCTTAT 358
Qy      360 CAGAGATGCGCGCT-GAGTGAAGAGGCGCTTGGGTTTAAGCTTTCAGTGCAGAA 418
Db      359 CAGAGATGCGCGCTGAGTGAAGAGGCGCTTGGGTTTAAGCTTTCAGTGCAGAA 418
Qy      419 GAAAGGTTACGTTAATATGATGATCATGACGATATGACAGAGAGAGCAGCGGCTA 478
Db      419 GAAAGGCTCTCTTAATATGATGATCATGACGATATGACAGAGAGAGCAGCGGCTA 478
Qy      479 ACTACGTGACAGAGCGCGGTTAATACGTAAGGCTGCAAGCTTAAATCGAATTAATCTGGGC 538
Db      479 ACTACGTGACAGAGCGCGGTTAATACGTAAGGCTGCAAGCTTAAATCGAATTAATCTGGGC 538
Qy      539 GTAAGGAGTGGAGCGGCTTGTAACTCAATGTAATCCCGGCTTAACCTGAG 598
Db      539 GTAAGGAGTGGAGCGGCTTGTAACTCAATGTAATCCCGGCTTAACCTGAG 598
Qy      599 ATTGCGTTTGAATCAAGAGCTAAGTGTGCAAGAGGAGGTGAAATTCATGTGTAC 658

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Db 599 ACGGCTTTGATGCTGCAAGGCTGAGTGGCGGCAAGGGGATGGAATTCGCGGTGAC 658
Qy 659 AGTGAATGCTGATGATGATGGAAGACATGATGCGGCAAGGCTGCTGGTTAAACA 718
Db 659 AGTGAATGCTGATGATGCGGAGGACACGATGGCGAAGGCAATCCCTGGGCTTCA 718
Qy 719 CTGAGGCTGATGCAAGGAGGTGGGGAGCAAGAGATTGATACCTGTGATGCCAG 778
Db 719 CTGAGGCTGATGCAAGGAGGTGGGGAGCAAGAGATTGATACCTGTGATGCCAG 778
Qy 779 CCCTAAAGCATGTCATAGTGTGTTGGGCTTATTAAGGCTGGTAACGATGACGCGT 838
Db 779 CCCTAAAGCATGTCATAGTGTGTTGGGCTTATTAAGGCTGGTAACGATGACGCGT 838
Qy 839 GAAGTTGACGCTGGGAGTACGCTGCGAAGATTAAATCTCAAGAAATGACGGGAC 898
Db 839 GAAGTTGACGCTGGGAGTACGCTGCGAAGATTAAATCTCAAGAAATGACGGGAC 898
Qy 899 CCGGCAAGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
Db 899 CCGGCAAGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
Qy 959 TTGACATGATGCAAGATTTTCTAGAGATAGATTAGTCT---TCGGGAGCGTTAACA 1015
Db 959 TTGACATGATGCAAGATTTTCTAGAGATAGATTAGTCTGAAAGAACTGACACAG 1018
Qy 1016 TGCTGATGCTGTGCTGAGCTGCTGTGCTGATGATGTTGGTTAACTCCGCAAGAG 1075
Db 1016 TGCTGATGCTGTGCTGAGCTGCTGTGCTGATGATGTTGGTTAACTCCGCAAGAG 1078
Qy 1076 CAACCTTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
Db 1076 CAACCTTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
Qy 1136 AACCGAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1195
Db 1136 AACCGAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1195
Qy 1196 GCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1253
Db 1196 GCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1253
Qy 1256 GCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1315
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Qy 1316 ATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1375
Db 1316 ATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1375
Qy 1376 ACCATGAGAGTGGGTTTCCACCAAGAGATGATGATGATGATGATGATGATGAT 1435
Db 1376 ACCATGAGAGTGGGTTTCCACCAAGAGATGATGATGATGATGATGATGATGAT 1435
Qy 1436 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1495
Db 1436 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1495
Qy 1495 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1553
Db 1495 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1553

RESULT 9
US-08-114-695A-8
Sequence 8, Application US/08114695A
Patent No. 5508193
GENERAL INFORMATION:
APPLICANT: Mandelbaum, Raphael T.
APPLICANT: Mackey, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
STREET: 3500 IDS CENTER

CITY: MINNEAPOLIS
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUEHLING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600,268US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
ORIGINAL SOURCE:
ORGANISM: Pseudomonas cepacia
US-08-114-695A-8

Query Match 75.1%; Score 1094.2; DB 2; Length 1474;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 992; Conservative 248; Mismatches 203; Indels 9; Gaps 3;
Qy 1 ATGGAAGCTGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 59
Db 28 AUNNAAGCTGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 87
Qy 60 TCTGTGCGGATGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 119
Db 88 ACCUGGCGGATGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 147
Qy 120 AACGATGAGGATGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 179
Db 148 AGCGGCGGATGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 207
Qy 180 AGACCTGCGCTTTGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGAT 239
Db 208 GGGGCTGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGAT 267
Qy 240 CCAAGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 299
Db 268 CCAAGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 327
Qy 300 GGGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 359
Db 328 GGGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 387
Qy 360 CCAAGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 419
Db 388 CCAAGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 447
Qy 448 AAUUCCTGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGAT 507
Db 480 CTAAGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 539
Qy 508 CTAAGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 567
Db 540 TAAAGGCGGATGAGAGCGGATGCTTTACATGATGATGATGATGATGATGATGATGATGAT 599

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Db      568 UAAAGCGUCGCGAGCGGUGUCUAGACCGAUGUAAUCCCGGGGCUCAACUUGGAA 627
Qy      600 TTGCGTTTGAATCTACAGGCTAGAGTGTGGCAGAGGAGTGAATTCATGTGATGA 659
      628 CUGCAUUGUGACUGGCGAGCUAGAGUAGNNAGAGGGGGUAGAUUCCAGCUAGAGA 687
Qy      660 GTGAAATGCGTGAATATGAGAAACATCGATGGGAAAGCGCTCTCTGGTTAAAC 719
      688 GUGAAUUGGUGAGAGUUGGAGAGAAUACCGAGGCGAAAGCGCCCGGCGCAUUD 747
Qy      720 TACAGCTGATGACGAAAGCGTGGGAGGAGAAACAGGATTAGATACCTGTAGTCAAC 779
      748 UACAGCUCUACGCAAGAGCGUGGAGGAGCAACAGAGUAGUACCTUGUAGUACAC 807
Qy      780 CTTAAACGATGTCATCTATGTTGGGCTTATTTAGGCTTGTGTAACGAACCTAAC 839
      808 CUUAAACGAGUACACUAGUUGUUGGAGAUUUCUUCUAGUAGUAGUAGUAGUAGU 867
Qy      840 AAGTTGACCGCTGGGAGATACGCTGCGAAGATTAATCTCAAGAGATTTAGAGGG 899
      868 AAGUUGACCGCGGAGGAGUACCGUUGCAAGAUUAAACUCAAAGAGAUUGACGG 927
Qy      900 CGCACAAGCGGAGTATGATGATTAATTCATGACGCGAAACCTTACCTTACCT 959
      928 CGCACAAGCGGAGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 987
Qy      960 TGACATGATGCAATTTTCTAGATAGATTAATGATGCT--TCGGAAACGCTAAC 1016
      988 UACACAGUUGCGAGUACUGUAGAGCGGAGAGUUGUCUCAAAGAACCGCGCA 1047
Qy      1017 GCTGCATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
      1048 GCGUACUGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
Qy      1077 AACCTTGTCTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1136
      1108 AACCTTGTCTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1162
Qy      1137 ACCGGAAGAGTGGGAGTACGCTCAAGTCTTATGCTGCTGCTGCTGCTGCTGCT 1196
      1163 ACCGGAAGAGTGGGAGTACGCTCAAGTCTTATGCTGCTGCTGCTGCTGCTGCT 1222
Qy      1197 GTAATCAATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1256
      1223 GUCAUACAUGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1282
Qy      1257 CGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
      1283 CGGAGUGGAGTGGGAGTACGCTCAAGTCTTATGCTGCTGCTGCTGCTGCTGCT 1342
Qy      1317 TCGCGATGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1376
      1343 UCGCGAGUACGAGUACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1402
Qy      1377 CCATGGAGTGGGTTTCAACGAAGAGATGCTTACCTTACCTTACCTTACCTTAC 1436
      1403 CCAUGGAGUUGGUGUACCAAGAGUUGGCUUACCAAGAGAGANNUGCACANANG 1462
Qy      1437 GTGAGATTGATG 1448
      1463 GUGAGAUUNANG 1474

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RESULT 10
US-09-735-567-6/c
; Sequence 6, Application US/09735567
; Patent No. 6508190
; GENERAL INFORMATION:
; APPLICANT: Brumecel, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; FILE REFERENCE: BCI033 US NA
; CURRENT APPLICATION NUMBER: US/09/735,567

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; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Unknown Organism
; OTHER INFORMATION: Description of Unknown Organism: Brachyomonas
; OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain R45
US-09-735-567-6

Query Match 74.2%; Score 1080.8; DB 3; Length 1539;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 1251; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

Qy      3 TGAAGCTGGCGGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 62
Db      1538 TGAAGCTGGCGGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1481
Qy      63 GGTGCGAGTGGCGGAGCGGAGTGAATGATGATGATGATGATGATGATGATGATGAT 122
Db      1480 GGTGCGAGTGGCGGAGCGGAGTGAATGATGATGATGATGATGATGATGATGATGAT 1421
Qy      123 GCATGGAAGATGCTTAAATACCGCATATCTTAAAGAGAGAGAGAGATC--GAA 180
Db      1420 TCGGGAAGAGCGGATTAATACCGCATATCTTAAAGAGAGAGAGAGATC--GAA 1361
Qy      181 GACCTTGGGCTTTTGGAGCGGCGGAGTCTGATGATGATGATGATGATGATGATGATGAT 240
Db      1360 GACCTTGGGCTTTTGGAGCGGCGGAGTCTGATGATGATGATGATGATGATGATGATGAT 1301
Qy      241 CAAGCGACATCACTAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db      1300 CAAGCGACATCACTAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1241
Qy      301 GCCGAGATCTCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db      1240 GCCGAGATCTCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1181
Qy      361 CAGCAATGCGGCGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db      1180 CAGCAATGCGGCGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1121
Qy      421 AAGGCTACGTAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db      1120 AAGGCTACGTAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1061
Qy      481 TACGTGCAAGAGCGGCGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db      1060 TACGTGCAAGAGCGGCGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1001
Qy      541 AAGGCTGCGAGAGGCGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 600
Db      1000 AAGGCTGCGAGAGGCGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 941
Qy      601 TCGCTTGAATCTACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
Db      940 TCGCTTGAATCTACAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 881
Qy      661 TGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db      880 TGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
Qy      721 GAGCTCATGACGAAAGCGTGGGAGCAACAGGATGATGATGATGATGATGATGATGATGATGAT 780
Db      820 GAGCTCATGACGAAAGCGTGGGAGCAACAGGATGATGATGATGATGATGATGATGATGATGAT 761
Qy      781 CTAAACGATGCTAAGTGTGGGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db      760 CTAAACGATGCTAAGTGTGGGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 701

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QY	1077	AACCTTGATTAATTAATGGCATACATTTGGTGGGACCTTAAATAGACATGGCGGTGCAA	1136
Db	1079	AACCTTGCCATCACTTGTCTACGAAA-----GGGCACTCTAATGGAGCATGGCGGTGACAA	1133
QY	1137	ACCGGAGGAAGGTGGGGATGACGTCAAGTCTCTCATGGCCCTTATGGTAGGGCTTCACAC	1196
Db	1134	ACCGGAGGAAGGTGGGGATGACGTCAAGTCTCTCATGGCCCTTATAGGTGGGGCTTACACAC	1193
QY	1197	GTAATTACAATGGCGCGTACAGAGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAG	1256
Db	1194	GTCAATTACAATGGCGGTACAAAGGGCAGCGAAAGCCGCGAAGGTGAAGCCAAATCCATTAAG	1253
QY	1257	CGCGTCGAGTCCGGATGCGAGTGCACACACGACTCCGTGAAGTCGGAAATCCGTCAGTAA	1316
Db	1254	CGCGTCGAGTCCGGATGCGAGTGCACACTCGACTGCTGAAGTCGGAATCCGTCAGTAA	1313
QY	1317	TGCGCGATACAGCATGTGCGCGGTGAATACGTTCCCGGGCTCTTGTAACAACCGCCCGTACA	1376
Db	1314	TGCGTGAATCAGCATGTCACGGTGAATACGTTCCCGGGCTCTTGTAACAACCGCCCGTACA	1373
QY	1377	CCATGGAGTGGGTTTCAACGAAAGCAGTATGCTTAACCGTAAAGAGGGGCGCTTGCCACG	1436
Db	1374	CCATGGGAGCGGGCTCTCAACGAAAGCAGTATGCTTAACCGAAGAGGGGCGCTTGCCACG	1433
QY	1437	GTGAGATTCAATGACGCGGGTG	1457
Db	1434	GTGGGAGTTTCGTGACTGGGGTG	1454

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RESULT 12
US-09-735-567-2/c
Sequence 2, Application US/09735567
Patent No. 6608190
GENERAL INFORMATION:
APPLICANT: Bramucci, Michael
TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
TITLE OF INVENTION: Industrial wastewater Bioreactors
FILE REFERENCE: BC1033 US NA
CURRENT APPLICATION NUMBER: US/09/735,567
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/171,140
PRIOR FILING DATE: 16 DECEMBER 1999
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 1467
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Brachymonas
OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain NBYE113
US-09-735-567-2

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Query Match	74.1%	Score 1079.6;	DB 3;	Length 1467;
Best Local Similarity	85.6%	Pred. No. 0;		
Matches 1251; Conservative	0;	Mismatches 199;	Indels 12;	Gaps 4;

QY	ATTGAAGCTGGGGGAGTCTTTACATCGAAGTCGAAGCGGACGACGATGCTTCAT	60
Db	ATTGAAGCTGGGGGAGTCTTTACATCGAAGTCGAAGCGGACGACGATGCTTCAT	1465
QY	CTGGTGGCGAATGGCGGACGGGTAGTATCATTCGGAACCTATTCGAAGAAGGGGGGTA	120
Db	CTGGTGGCGAATGGCGGACGGGTAGTATCATTCGGAACCTATTCGAAGAAGGGGGGTA	1407
QY	ATGGCGGCGAATGGCGGACGGGTAGTATCATTCGGAACCTATTCGAAGAAGGGGGGTA	1348
Db	ATGGCGGCGAATGGCGGACGGGTAGTATCATTCGGAACCTATTCGAAGAAGGGGGGTA	1287
QY	ACGCATCGAAGAATGTCTTAATACCGCATATCTTAAAGAGGAAGCAGGGGA--TCGA	178
Db	ACGCATCGAAGAATGTCTTAATACCGCATATCTTAAAGAGGAAGCAGGGGA--TCGA	1288
QY	GCTGGCGGAAGCCGGAATTATATACCGCATGATCCGCGATGGAAGCAGGGGACTCGCA	1288
Db	GCTGGCGGAAGCCGGAATTATATACCGCATGATCCGCGATGGAAGCAGGGGACTCGCA	1288
QY	AAGACCTTGGCGCTTTTGGAGGCGCGCGAATGTGATTTAGCTAGTTGGTGGGTTAAGGCT	238
Db	AAGACCTTGGCGCTTTTGGAGGCGCGCGAATGTGATTTAGCTAGTTGGTGGGTTAAGGCT	1228

QY	239	ACCAAGCGACGATCACTACTTGGTCTGAGAGACGACACGACCACTGGGACTGAGACA	298
Db	1227	ACCAAGCTCGGACTCTGTACTGTGTCTGAGAGATGATCAGCCACATCGGGACTGAGACA	1168
QY	299	CGGCCCGACTCTACCGGAGGACGACGAGTGGGAAATTTGACATAGCGCGAAGCTTGA	358
Db	1167	CGGCCCGAATCTCTACCGGAGGACGAGTGGGGAATTTTGACATAGCGCGAAGCTTGA	1108
QY	359	TCCACGCAATCCGGGTGATGMAAGAGCCTTCGGGGTGTAAAGCTCTTCAGTCGAGAA	418
Db	1107	TCCACGCATCCGGGTGACAGATGMAAGCCTTCGGGGTGTAACTGCTTTTGTACGAAAC	1048
QY	419	GAAGAAGTTACGGTAATATCGGACTCATGACGGTATGACAGAAAGACACCGGCTA	478
Db	1047	GAAGAAGCTCTTTCTAATATAAGAGGGGACATGACGGTATGAAATATAGACCGGCTA	988
QY	479	ACTACGTCCAGCAGCCCGCGGTAAATAGTAGGGTGCACGCTTAATCGAAATTACTGGGC	538
Db	987	ACTACGTCCAGCAGCCCGCGGTAAATAGTAGGGTGCACGCTTAATCGAAATTACTGGGC	928
QY	539	GTAAAGGTCCGACAGGGGGCTTTGTATAGTACGATATGGAATATCCCGGGCTTAACCTGGGA	598
Db	927	GTAAAGGTCCGACAGGGGGCTTTGTCAAGACAGTGTGAATATCCCGGGCTCAACCTGGGA	868
QY	599	ATTGCGTTTAAACTACAGAGCTAGAGTGTGACAGAGGAGGTGGAATTCATATGTATAGC	658
Db	867	ACTGCCATTGTGACTGCAAGGCTGGAATACGGCAGAGGGGGATATGGAATTCGGGTGTATGC	808
QY	659	AGTGAATATGCTAGAGATATGAAAGACATCGATATGGCGAAGGCAGCCTCTCGGCTTAACA	718

Qy	1016	TGCTGCAATGGCTCTGCGCACTGCGTACGTAATGTGGGTTAAAGCCGCAACAGCG	1075
Db	447	TGCTGCAATGGCTCTGCGCACTGCGTACGTAATGTGGGTTAAAGCCGCAACAGCG	388
Qy	1076	CAACCCCTTGTCATTAATGGCAATTTGGTTGGGCACTTTAATGAGACTGCCGGTGACA	1135
Db	387	CAACCCCTTGTCATTAATGGCAATTTGGTTGGGCACTTTAATGAGACTGCCGGTGACA	333
Qy	1136	AACCGGAGGAAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTATGGGTAGGGCTTACA	1195
Db	332	AACCGGAGGAAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTATGGGTAGGGCTTACA	273
Qy	1196	CGTAATACAAATGGCGCGGTACAGAGGGTTGCAACCCGCGAGGGGAGACTAATCTCAGAAA	1255
Db	272	CGTAATACAAATGGCGCGGTACAGAGGGTTGCAACCCGCGAGGGGAGACTAATCTCAGAAA	213
Qy	1256	GGCGGTGATGATCCGGATGCGAATCTGCAACTCGATCCGTTGAAGTCGGAATGCGTAGTA	1315
Db	212	GGCGGTGATGATCCGGATGCGAATCTGCAACTCGATCCGTTGAAGTCGGAATGCGTAGTA	153
Qy	1316	ATGCGGATCAGCATGTCCGGGTGAATACGTTCCGGGTTCTTATACACACCGCCCGTCAC	1375

Db 1082 CAACCTTGCTCTAGTTC-----TAGCAAGACACTTAAGAGACCTGCCGGTACA 1136
Qy 1136 AACCGAGAGAGTGGGATGACGTCAATCTCTATGCGCTTATGGGTAGGGCTTACA 1195
Db 1137 AACCGAGAGAGTGGGATGACGTCAATCTCTATGCGCTTATGGGTAGGGCT-TCACA 1195
Qy 1196 GGTATTAACAATGGCGGTACAGAGGGTTGCCAACCGCGAGGGGAGTAACTCTAGAAA 1255
Db 1196 GGTATTAACAATGGCGGTACAGAGGGTTGCCAACCGCGAGGGGAGTAACTCTAGAAA 1254
Qy 1256 GCGCGTCTAGTCCGAGTCCGAGTCTGCAACTGCACTCCGTAAGTCGGAATCGTAGTA 1315
Db 1255 ACCGATCGTAGTCCGAGTCTGCAACTGCACTCCGTAAGTCGGAATCGTAGTA 1314
Qy 1316 ATCCGAGTACAGATGTCCGGTGAATAGCTTCCGGGTCTTGTACACACCCCGCTCAC 1375
Db 1315 ATCCGAGTACAGATGTCCGGTGAATAGCTTCCGGGTCTTGTACACACCCCGCTCAC 1374
Qy 1376 ACCATGGAGTGGTGTTCACAGAAAGAGTGTAGTCTAACCGTAAGG-AGGGCGTTGACA 1434
Db 1375 ACCATGGAGTGGTGTTCACAGAAAGAGTGTAGTCTAACCGTAAGGAGAGACGATCCCA 1434
Qy 1435 CGGTAGATTCATGACTGGG 1454
Db 1435 CGGTAGATTCATGACTGGG 1454

RESULT 15
US-09-228-184-1
; Sequence 1, Application US/09228184
; Patent No. 6322782
; GENERAL INFORMATION:
; APPLICANT: WALKER, Harrell L.
; INVENTOR: HIGGINBOTHAM, Lawrence R.
; TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
; FILE REFERENCE: 013243-0007
; CURRENT APPLICATION NUMBER: US/09/228,184
; CURRENT FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1540
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURES:
; OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3;
; OTHER INFORMATION: gram negative; rod-shaped; exhibits flagellate
; OTHER INFORMATION: motility; pathogenic to cyanobacteria and algae;
; OTHER INFORMATION: yellow colonies on BG-11 medium suppl. with tryptic
US-09-228-184-1

Query Match 72.3%; Score 1053; DB 3; Length 1540;
Best Local Similarity 84.7%; Pred. No. 0;
Matches 1242; Conservative 0; Mismatches 215; Indels 10; Gaps 5;

Qy 1 ATTGAACCTGGCGGCGATGCTTTACATGCAATGCAAGTCGAAACGGCAGACAGGATGCTTGAT 60
Db 24 AGTGAACCTGGCGGCGGAGGCTTAAACATGCAATGCAAGTCGAAACGGCAGACAGGATGCAAT 83
Qy 61 CT-----GGTGCAGATGCGGAGCGGAGTGAATGATGATGCAAGTATTCAGAAAGGGG 116
Db 84 ACTGGGGTGGCGATGGCGAGCGGGTGAAGAAATACATCGGAATCTGCCAGTCTGGGG 143
Qy 117 GGTAAACGATGAAAGATGTCTAATACCGCATATCTTAAGAGAGAAAGAGGGATC 176
Db 144 GATTAACATAGGAGAACTTATGTCTAATACCGCATATCGACTTAAGGGTGAAGCGGGGATC 203
Qy 177 GAAGAAGCTTGGGCTTTGGAGCGGCGAGTGTCTAATAGCTAGTGTGGGTAAAGG 236
Db 204 GGAAGACCTCGGCGATGAGTGAACCGATGTCGATTAAGTTGGCGGGTAAATGCG 263
Qy 237 CTACCAAGCGACATCATAGTGTGTCTGAGAGACGACCACTGGGACTGAGA 296

Db 264 CAACCAAGCGACATCGGTAGTGTCTGAGAGATGATCAGCACTGGAATCTGAGA 323
Qy 267 CACGGCCCAAGCTCTTACAGGAGACAGATGGGGAATTTGGACAATGGGCGAAGCT 356
Db 324 CACGGTCAAGCTCTTACAGGAGACAGATGGGGAATTTGGACAATGGGCGAAGCT 383
Qy 357 GATCCAGAAATGCGCGGATGAAGAAAGGCTTCGGGTGTAAAGCTCTTTCAGTCAG 416
Db 384 GATCCAGCAATGCGCGGATGAAGAAAGGCTTCGGGTGTAAAGCTCTTTCAGTCAG 443
Qy 417 AAGAAAGCTTACGGTAATTAATCTGTACTGATGACGGTATGACAGAAAGACACCGGC 476
Db 444 AAGAAAGCACTGATTAATTAATCTGTACTGATGACGGTATGACAGAAAGATTAAGCACCGGC 503
Qy 477 TAATAGTGGCAGACGCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 536
Db 504 TAATAGTGGCAGACGCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 563
Qy 537 GGTAAAGGGTGGCAGGCGGCTTGTAGTCAAGATGAAATCCCGGGCTTAACTGG 596
Db 564 GGTAAAGGGTGGCAGGCGGCTTGTAGTCAAGATGAAATCCCGGGCTTAACTGG 623
Qy 597 GAATTCGTTGAACTTCAAGAGCTAGTGGCAGAGGAGTGAATTCATGTGTA 656
Db 624 GAATTCGTTGAACTTCAAGAGCTAGTGGCAGAGGAGTGAATTCATGTGTA 683
Qy 657 GCATGAAATTCGATGATATGGAAGAACATTCATGCGCAAGGCAAGCTCTCGGTAA 716
Db 684 GCATGAAATTCGATGATATGGAAGAACATTCATGCGCAAGGCAAGCTCTCGGTAA 743
Qy 717 CACTGACGCTCATCAGAAAGCTGGGAGCAAAAGATTAATTAATTAATTAATTAATTAATTA 776
Db 744 CACTGACGCTCATCAGAAAGCTGGGAGCAAAAGATTAATTAATTAATTAATTAATTAATTA 803
Qy 777 CGCCCTTAACGATGCAATGATTTGGGCTTATTAGG--CTTGTACAGAACTAAC 834
Db 804 CGCCCTTAACGATGCAATGATTTGGGCTTATTAGG--CTTGTACAGAACTAAC 863
Qy 835 GCGTGAAGTTGACCGGCTGGGAGTACGCTGCGCAAGTAAATCTCAAAAGAAATTAAGG 894
Db 864 GCGTGAAGTTGACCGGCTGGGAGTACGCTGCGCAAGTAAATCTCAAAAGAAATTAAGG 923
Qy 895 GGAACCGCAAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 954
Db 924 GGAACCGCAAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 983
Qy 955 ACCCTTGAATGATGCAATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATG 1013
Db 984 GGCCTTGAATGATGCAATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATG 1043
Qy 1014 GGTGCTGATGCTGTGTGCTCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1073
Db 1044 GGTGCTGATGCTGTGTGCTCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1103
Qy 1074 CGCAACCTTGTCTAATTAATGCGCATCA--TTTGGTGGGCACTTAAATGAGATGCGCGGT 1131
Db 1104 CGCAACCTTGTCTAATTAATGCGCATCA--TTTGGTGGGCACTTAAATGAGATGCGCGGC 1163
Qy 1132 GACAAACCGAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1191
Db 1164 GACAAACCGAGAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1223
Qy 1192 CACACGTAATTAATGCGCGGTACAGAGGTTGGCAACCGCGAGGGGAGTAACTCA 1251
Db 1224 CACACGTAATTAATGCGCGGTACAGAGGTTGGCAACCGCGAGGGGAGTAACTCA 1283
Qy 1252 GAAAGCGCTGTAGTCCGAGTCCGAGTCTGCAACTGCACTCCGAGTGAAGTGAATGCT 1311
Db 1284 GAAAGCGCTGTAGTCCGAGTCCGAGTCTGCAACTGCACTCCGAGTGAAGTGAATGCT 1343
Qy 1312 AGTAATGCGGATGACA-TGTGCGGTGAATACGTTCCGGGTCTTGTACACACCGCC 1370
Db 1344 AGTAATGCGGATGACA-TGTGCGGTGAATACGTTCCGGGTCTTGTACACACCGCC 1403

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Oy 1371 GTGACACCATGGGAGTGGTTTACCAAGACGTAAGTCTAACCGTAAGAGAGGCGCTT 1430
    |||||
Db 1404 GTGACACCATGGGAGTGGTTTGTGACACCAAGACGTAAGTCTTAACCGAAGGGGGCGCTT 1463
    |||||
Oy 1431 GCCACGGTGAGATTCAATGACTGGGGTG 1457
    |||||
Db 1464 GCCACGGTGAGATTGACTGGGGTG 1490
    |||||

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Search completed: April 6, 2006, 21:34:17
 Job time : 257 secs

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